

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 15, 2003, 19:38:05 : Search time 299 Seconds  
(without alignments)  
1852.815 Million cell updates/sec

Title: US-10-036-041-2  
Perfect score: 1367  
Sequence: 1 MLMROLIYQMLAFLFLPC.....LHGHDHRETFAGFLLETK 246

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 218539 segs, 112599159 residues  
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q/cg2.1/USPTO.spool/US10036041/rnat\_13012003\_160808\_7048/app-query.fasta.1.391  
-DB=N.Geneseq.101002 -QPMT=fastlap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdl  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTPMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10036041.ecgn.1.1.79\_etunat\_13012003\_160808\_7048 -NCPU=6 -ICPU=3  
-NO\_XLPHY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-MARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N.Geneseq.101002:\*  
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21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID    | Description         |
|------------|--------|-------------|--------|----------|---------------------|
| 1          | 1367   | 100.0       | 741    | ABK35591 | Gene encoding nove  |
| 2          | 1367   | 100.0       | 1696   | ABK64058 | Human zacr3p cDNA,  |
| 3          | 1367   | 100.0       | 1709   | AAK93874 | Human cDNA encodin  |
| 4          | 1367   | 100.0       | 1712   | AAA96336 | cDNA encoding a no  |
| 5          | 1367   | 100.0       | 1760   | AAA95787 | Human immune syste  |
| 6          | 1320.5 | 96.6        | 960    | ABK35590 | Gene encoding nove  |
| 7          | 1311   | 95.9        | 1035   | AAK9976  | Skin cell cDNA, SE  |
| 8          | 1311   | 95.9        | 1035   | ABK34928 | Rat cDNA isolated   |
| 9          | 1311   | 95.9        | 1117   | AAK64064 | Mouse zacr2 DNA,    |
| 10         | 1311   | 95.9        | 1123   | AAK61633 | cDNA encoding rat   |
| 11         | 1311   | 95.9        | 1123   | AAK61730 | cDNA encoding rat   |
| 12         | 1311   | 95.9        | 1123   | AAK99566 | Skin cell cDNA, SE  |
| 13         | 1311   | 95.9        | 1123   | AAK99663 | Skin cell cDNA, SE  |
| 14         | 1311   | 95.9        | 1123   | ABK34718 | Rat cDNA isolated   |
| 15         | 1311   | 95.9        | 1123   | ABK34815 | Rat cDNA isolated   |
| 16         | 1291.5 | 94.5        | 1927   | AAK12584 | Human protein havi  |
| 17         | 1259   | 92.1        | 810    | AAK94076 | Primer specific fo  |
| 18         | 1211   | 88.6        | 1792   | AAK59230 | Human polynucleot   |
| 19         | 1208   | 88.4        | 1620   | AAK95523 | Human polynucleot   |
| 20         | 1171   | 85.7        | 738    | AAK64063 | Human zacr3p degen  |
| 21         | 858.5  | 62.8        | 1799   | AAK61016 | Human polynucleot   |
| 22         | 849    | 62.1        | 1608   | ABK35221 | Human cDNA encodin  |
| 23         | 721    | 52.7        | 471    | AAK02874 | Human secreted pro  |
| 24         | 721    | 52.7        | 472    | AAK39551 | Human secreted pro  |
| 25         | 513.5  | 37.6        | 546    | AAK93419 | cDNA encoding SRT   |
| 26         | 325    | 23.8        | 804    | ABK35598 | Gene encoding nove  |
| 27         | 316    | 23.1        | 1107   | AAK61744 | cDNA encoding rat   |
| 28         | 316    | 23.1        | 1107   | AAK99677 | Skin cell cDNA, SE  |
| 29         | 316    | 23.1        | 1107   | ABK34829 | Rat cDNA isolated   |
| 30         | 315    | 23.0        | 870    | AAK16359 | Human SBAKRP30a g   |
| 31         | 315    | 23.0        | 870    | ABK08182 | Human SBAKRP30a g   |
| 32         | 315    | 23.0        | 912    | AAK16351 | Novel human gene.   |
| 33         | 315    | 23.0        | 912    | AAK09867 | Human SBAKRP30a g   |
| 34         | 315    | 23.0        | 1242   | AAK44067 | Human zacr3p cDNA,  |
| 35         | 315    | 23.0        | 1297   | ABK4966  | Human genseit metab |
| 36         | 313    | 22.9        | 855    | AAK67788 | Human novel polynu  |
| 37         | 309    | 22.6        | 1282   | AAK98975 | Murine ACRP30RIM c  |
| 38         | 306    | 22.4        | 1052   | AAK61811 | Mouse zacr3p cDNA,  |
| 39         | 306    | 22.4        | 1052   | AAK99744 | cDNA encoding rat   |
| 40         | 306    | 22.4        | 1052   | ABK34896 | Skin cell cDNA, SE  |
| 41         | 306    | 22.4        | 1161   | AAK65132 | Rat cDNA isolated   |
| 42         | 306    | 22.4        | 1171   | AAK51128 | Human adipocyte co  |
| 43         | 306    | 22.4        | 1171   | ABK04564 | Human diagnostic a  |
| 44         | 304    | 22.2        | 932    | AAK25606 | Human ovarian anti  |
| 45         | 299    | 21.9        | 1276   | AAK51048 | cDNA encoding poly  |
|            |        |             |        |          | Murine adipocyte c  |

## ALIGNMENTS

RESULT 1  
ABK35591  
ID ABK35591 standard; DNA; 741 BP.

XX ABK35591:

DT 08-MAY-2002 (first entry)

DE Gene encoding novel human secreted or membrane-associated protein #10.

XX Human; secreted protein; membrane-associated protein; hypertension;

KW inflammatory disorder; neurological disorder; haematopoietic disorder;

KW skeletal developmental disorder; growth abnormality; autoimmune disorder;

KW neurodegenerative disorder; nervous system disorder; bacterial infection;

KW peripheral myelinopathy; viral infection; cancer; obesity; diabetes;

OS hypotension; sexual development disorder; blood disorder; gene; ds.

XX Homo sapiens.

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XX  MO200204600-A2.
PN
XX
XX  17-JAN-2002:
PD
XX
XX  12-JUL-2001: 2001MO-US21985.
PF
XX
XX  12-JUL-2000: 2000US-218033P.
PR
XX  21-AUG-2000: 2000US-226517P.
PR
XX
XX  (SMIR ) SMITHKLINE BEECHAM CORP.
PA  (SMIR ) SMITHKLINE BEECHAM PLC.
PA  (GLAX ) GLAXO GROUP LTD.
XX
XX  Agarwal P, Cogswell JP, Lai Y, Martensen SA, Rizvi SK, Strum JC;
PI  Smith RF, Xiang Z, Xie Q;
XX
XX  WPI: 2002-188468/24.
DR  P-PSDB; AAU84371.
XX
XX  Novel secreted and membrane-associated polypeptides and polynucleotides
PT  encoding the polypeptides, for preventing, treating and ameliorating
PT  cancers, mental or sexual developmental disorders, and malignant tumours
PT
XX
XX  Claim 2: Page 106; 151pp; English.
PS
XX
XX  The present invention relates to the isolation of novel human secreted
CC  or membrane-associated proteins and the genes encoding them. The
CC  sequences of the invention are useful for treating, preventing and
CC  ameliorating various diseases such as inflammatory disorders (e.g.
CC  asthma), neurological disorders (e.g. dementia), haematopoietic
CC  disorders, skeletal developmental disorders, growth abnormalities,
CC  neurodegenerative disorders (e.g. Huntington's disease), nervous system
CC  disorders, autoimmune disorders (e.g. rheumatoid arthritis),
CC  peripheral myelinopathies, viral and bacterial infections,
CC  alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and
CC  hypotension, obesity, bulimia, anorexia, manic depression, delirium,
CC  mental retardation, Tourette's syndrome, schizophrenia, growth, mental
CC  or sexual development disorders, and dysfunction of the blood cascade
CC  system including those leading to stroke. ABK3582-ABK35609 represent
CC  the genes encoding the novel human secreted or membrane-associated
CC  proteins of the invention.
XX
XX  Sequence 741 BP; 191 A; 178 C; 200 G; 172 T; 0 other:
SQ
XX
XX  Alignment Scores:
XX  Pred. No.: 7.45e-100 Length: 741
XX  Score: 1367.00 Matches: 246
XX  Percent Similarity: 100.00% Conservative: 0
XX  Best Local Similarity: 100.00% Mismatches: 0
XX  Query Match: 100.00% Indels: 0
XX  DB: 24 Gaps: 0
XX
XX  US-10-036-041-2 (1-246) x ABK35591 (1-741)
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XX  1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPheLeuProPheCys 20
XX  |||||||
XX  1 ATGCTTTGGAGCAGCATCATCTATGCACTGCTGCTTTGTTTCCCTCTTTTGC 60
XX  |||||||
XX  21 LeuCysGlnAspGlnuTyrMetGlnuSerProGlnThrGlyGlyLeuProProAspCysSer 40
XX  |||||||
XX  61 CTGTGTCATAAGATGATGATGAGTCTCCACAACCGGAGAGATACCCCAAGACTGCAGT 120
XX  |||||||
XX  41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
XX  |||||||
XX  121 AAGTGTTGTCATGAGAGCTACAGCTTTCGAGGCTACCAAGGCCCTTGCGCCACCGGCG 180
XX  |||||||
XX  61 ProProGlyLyleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
XX  |||||||
XX  181 CCTCTGGCATTCACAGAAACCATGCAATGCAACATGAGGACACTGGTCAATGAA 240
XX  |||||||
XX  81 GlyAlaLysGlyGlyLysGlyAspLysGlyAspLeuGlyProArgGlyAlaGlyGlyGln 100

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DB  241 GGAGCCAAAGGTGAGAGAGGCGACAAAGGTGACCTGGGGGCTTGAGGGGAGCGGGCAG 300
XX  |||||||
XX  101 HisGlyProLysGlyGlyLysGlyTyrProGlyLyleProProGlnLeuGlnIleAlaPhe 120
XX  |||||||
XX  301 CATGGCCCCCAAGAGAGAGAGGCGTACCCGGGATTCACACAGACTTCAGATTGCATTC 360
XX  |||||||
XX  121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyLylePheSerVal 140
XX  |||||||
XX  361 ATGCTTCTCTGCGCAACCCCTTCACGAATCAGAACAGTGGATATTCTTCACACAGTGT 420
XX  |||||||
XX  141 GluThrAsnIleGlyAsnIlePheAspValMetThrGlyArgPheGlyAlaProValSer 160
XX  |||||||
XX  421 GAGACCAACATGTGAAACTTCTTGATGTCATGATGATGATTTGGGCCCAAGTATCA 480
XX  |||||||
XX  161 GlyValTyrPhePheThrPheSerMetMetLysHisGlyAspValGluGlyValTyrVal 180
XX  |||||||
XX  481 GGTGTGATTTCTTCACCTTCACACATGATGATGATGATGATGATGATGATGATGAT 540
XX  |||||||
XX  181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetCysTyrGlyMetLysGlyLys 200
XX  |||||||
XX  541 TACCTTATGCAATGAGCAACAGAGCTTTCACATGATGATGATGATGATGATGATGAT 600
XX  |||||||
XX  201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPleu 220
XX  |||||||
XX  601 TCAGATTCATCCAGCAATCATGCTGTGCTTAAGCTAAGCAAGGGGATGAGTTGGCTG 660
XX  |||||||
XX  221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
XX  |||||||
XX  661 CGAATGGCGAATGAGCGCTGCCATGGGACACCAACGCTTCCACCTTGGCAGGATTC 720
XX  |||||||
XX  241 LeuLeuPheGluThrLys 246
XX  |||||||
XX  721 CTGCTCTTTGAAACTAAG 738
XX
XX  RESULT 2
XX  AAC64058
XX  ID AAC64058 standard; cDNA; 1696 BP.
XX
XX  AAC64058:
XX
XX  19-FEB-2001 (first entry)
XX
XX  Human zacr3 cDNA, SEQ ID NO:1.
XX
XX  Human zacr3; adipocyte complement related protein homologue;
XX  ACRP30; C1q domain; collagen-like domain; energy balance modulation;
XX  cellular metabolism; metabolic disorder; obesity; anorexia;
XX  antimicrobial agent; infection; platelet aggregation inhibition;
XX  adhesion; activation; vascular injury; antibacterial; antiviral; ss.
XX
XX  Homo sapiens.
XX
XX  MO200063377-A1.
XX
XX  26-OCT-2000.
XX
XX  19-APR-2000: 2000MO-US10454.
XX
XX  20-APR-1999: 99US-0294943.
XX
XX  (ZYMO ) ZYMOGENETICS INC.
XX
XX  Piddington CS, Bishop PD;
XX
XX  WPI: 2000-665243/64.
XX  P-PSDB; AAB29580.
XX
XX  Novel zacr3 polypeptides used to treat or prevent bacterial or viral
XX  infections, for wound healing, improving blood flow, and to analyze
XX  energy efficiency in mammals -
XX
XX  Claim 31: Page 107-109; 123pp; English.
PS

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|   |   |
|---|---|
| XX  | The invention relates to the human zacr3 protein (AAB29580) and to        |
| CC  | nucleic acids which encode it (AAC64058, AAC64063). Zacr3 is a homologue  |
| CC  | of adipocyte complement related protein (ACRP30) and contains a           |
| CC  | collagen-like domain comprising gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a |
| CC  | C-terminal C1q domain comprising 10 beta-strands. The zacr3 gene is       |
| CC  | located on chromosome 5p12. The invention also relates to zacr3           |
| CC  | fragments, fusion proteins containing zacr3 polypeptides,                 |
| CC  | zacr3-specific antibodies, expression constructs and host cells           |
| CC  | comprising zacr3 nucleic acids, and methods of recombinant production of  |
| CC  | zacr3. Human zacr3, and its agonists and antagonists may be used in the   |
| CC  | study and modulation of cellular metabolism and energy balance in         |
| CC  | mammals, and may therefore be used to treat disorders such as obesity and |
| CC  | anorexia, and conditions associated with these disorders. Due to its C1q  |
| CC  | like domain, zacr3 and zacr3-containing fusion proteins may be useful     |
| CC  | as antimicrobial agents, promoting lysis or phagocytosis of infectious    |
| CC  | organisms such as bacteria or viruses. Zacr3, its fragments, fusion       |
| CC  | proteins, antibodies and activity modulators may also be used to inhibit  |
| CC  | collagen-induced platelet aggregation, adhesion, or activation, and may   |
| CC  | therefore have potential for promoting blood flow within the vasculature  |
| CC  | of a mammal e.g., to treat injury to the vasculature or other collagenous |
| CC  | tissue. Human zacr3 and its antibodies may additionally be used to study  |
| CC  | dimetrisation and oligomerisation. The present sequence represents cDNA   |
| CC  | encoding human zacr3.   |
| XX  |   |
| S0  | Sequence 1696 BP; 482 A; 355 C; 386 G; 473 T; 0 other;                    |
| Alignment Scores:                           |   |
| Pred. No.:                                  | 1.94e-99 Length: 1696   |
| Score:                                      | 1367.00 Matches: 246  |
| Percent Similarity:                         | 100.00% Conservative: 0   |
| Best Local Similarity:                      | 100.00% Mismatches: 0   |
| Query Match:                                | 100.00% Indels: 0   |
| DB:   | 21 Gaps: 0  |
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| OY  | 1 MetLeuTPraTgInLeuIleIeTYrTPGInLeuAlaLeuPheLeuProPheCys 20               |
| DB  | 69 ATGCTTTGGAGGCGACGCATCTTTGGCAACGTCGTGCTTTTCTCCTTTTTC 128                |
| OY  | 21 LeuCysGlnAspGluTYrMetGluSerProGlnThrGlyLeuProPheCysPcysSer 40          |
| DB  | 129 CTGTGTCAAATGATGATCATGTGAGTCTCCACAAACGGGAGCACTCCCGACAGTCGAGT 188       |
| OY  | 41 LysGlyCysHisGlyAspTYrSerPheArgGlyTYrGlnGlyProProGlyProProGly 60        |
| DB  | 189 AAGGTGTGTCATGAGATCTACAGCTTTCAGAGCTCTCAAGAGCCCTCCGTGGCCACCGGGC 248     |
| OY  | 61 ProProGlyLLeProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80        |
| DB  | 249 CTCCTGCGCATTCAGGAAACCATGGAACCATGGCAACATGAGAGCCACATGCTCATGAA 308       |
| OY  | 81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100       |
| DB  | 309 GAGAGCCAAAGGTAGAAGGCGCAGCAAAAGGTGACCTGGGGCCCTCGAGGGAGAGCGGGCGAG 368   |
| OY  | 101 HisGlyProLysGlyGluLysGlyTYrProGlyLLeProProGlnLeuGlnIleAlaPhe 120      |
| DB  | 369 CATGGCCCCAAGAGAGAAAGGGCTACCCGGGGGATTCCACCAAGAACTTCAATATGCAATTC 428    |
| OY  | 121 MetaLaserLeuAlaThrHisPheSerAsnGlnAsnSerGlyLleIlePheSerSerVal 140      |
| DB  | 429 ATGAGCTCTCTCGCAACCCACTTCACGATTCAGAAACAGTGGGATTTCTTCAGCAGTGT 488       |
| OY  | 141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160      |
| DB  | 489 GAGACCAACATTTGGAAACTCTTGTATGTCAAGACTGTGATGATTTGGGGCCCGCCAGTATCA 548   |
| OY  | 161 GlyValLysPhePheThrPheSerMetMetLysHisGlyAspValGluGlnValTYrVal 180      |
| DB  | 549 GGTGTGATTTCTTCACCTTCACAGATGATGAAGCATGAGAGATGTTGACAGAAAGTATATGTG 608   |

|          |             |   |     |
|----------|-------------|---|-----|
| Oy       | 181         | TyLeuNethIaNsngIyAsnTrVAlPheSerMeTtySeTtyGlMeTlySgIyys                    | 200 |
| Oy       | 181         | TyLeuNethIaNsngIyAsnTrVAlPheSerMeTtySeTtyGlMeTlySgIyys                    | 200 |
| Db       | 609         | TACCTTATGCAACATGGCAACACAGCTTCACAGTGTACAGCTAAGAATAAGGCAAA                  | 668 |
| Oy       | 201         | SerAspPheSerSerAsnHISAlaValLeuLysLeuAlaLysGlyAspG1ValTrPheU               | 220 |
| Db       | 669         | TCAATATACATCCAGCATATCTGCTGTGCTGAAGCTAAGCAAGGGGATGAGGTTTGCTG               | 728 |
| Oy       | 221         | ArgMeTlyAsnGlyAlaLeuHISGlyAspHISGlyAspHISGlyAspSerThrPheAlaGlyPhe         | 240 |
| Db       | 729         | CGAATGGGCAATGGCGCTCTCCATGGGAGCAACAAAGCTTCTCACCTTTGACGATTC                 | 788 |
| Oy       | 241         | LeuLeuPheG1urThrIys   | 246 |
| Db       | 789         | CTGCTCTTGAACCTAAG   | 806 |
| RESULT 3 |             |   |     |
| ID       | AAAF93874   | standard; cDNA; 1709 BP.  |     |
| XX       | AAAF93874:  |   |     |
| AC       |             |   |     |
| XX       | 23-MAY-2001 | (first entry)   |     |
| DT       |             |   |     |
| XX       |             |   |     |
| DE       |             | Human cDNA encoding a membrane or secretory protein clone PSEC0232.       |     |
| XX       |             |   |     |
| KW       |             | Human; secretory protein; membrane protein; vaccine; gene therapy;        |     |
| KW       |             | rheumatoid arthritis; diabetes; ss.                                       |     |
| OS       |             | Homo sapiens.   |     |
| XX       |             |   |     |
| PN       |             | EP1067182-A2.   |     |
| PD       |             | 10-JAN-2001.  |     |
| XX       |             |   |     |
| PE       |             | 07-JUL-2000; 2000EP-0114090.  |     |
| XX       |             |   |     |
| PR       |             | 08-JUL-1999; 99JP-0194179.  |     |
| PR       |             | 11-JAN-2000; 2000JP-0118775.  |     |
| XX       |             | 02-MAY-2000; 2000JP-0183766.  |     |
| PR       |             |   |     |
| PA       |             | (HELI-) HELIX RES INST.   |     |
| XX       |             |   |     |
| PI       |             | Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;             |     |
| XX       |             |   |     |
| DR       |             | WPI: 2001-093989/11.  |     |
| DR       |             | P-PSDB; AAB88447.   |     |
| XX       |             |   |     |
| PS       |             | Claim 1; SEQ ID 261; 609pp + CD ROM; English.                             |     |
| CC       |             | This invention relates to nucleic acid sequences AAf93744 - AAf93916      |     |
| CC       |             | which encode human secretory or membrane proteins represented by          |     |
| CC       |             | AAB88317 - AAB88419. Included in the invention are primers                |     |
| CC       |             | AAf93917 - AAf94295 and AAf62232 - AAf62235 which are used to isolate the |     |
| CC       |             | cDNA sequences of the invention. The invention also includes methods for  |     |
| CC       |             | the production of antibodies directed against the proteins, and cDNA      |     |
| CC       |             | sequences, which can be used in vaccines. The polynucleotide sequences    |     |
| CC       |             | can be used in gene therapy. The polynucleotide sequences and the         |     |
| CC       |             | proteins they encode may be used in the prevention, treatment and         |     |
| CC       |             | diagnosis of diseases associated with inappropriate secretory             |     |
| CC       |             | protein/membrane protein expression. The nucleic acids and complementary  |     |
| CC       |             | sequences may also be used as DNA probes in diagnostic assays             |     |
| CC       |             | (e.g. polymerase chain reactions (PCR)) to detect and quantitate the      |     |
| CC       |             | presence of similar nucleic acid sequences in samples. They may also be   |     |
| CC       |             | used to study the expression and function of secretory proteins/membrane  |     |
| CC       |             | polypeptides and their role in metabolism. The polypeptides may be used   |     |
| CC       |             | as antigens in the production of antibodies against them and in assays to |     |
| CC       |             | identify modulators (agonists and antagonists) of expression and          |     |
| CC       |             | activity. The antibodies and antagonists may also be used as therapeutic  |     |
| CC       |             | agents to down regulate expression and activity. The antibodies may also  |     |



CC dermatitis herpeticiformis or Crohn's disease. The nucleic acids may be used  
 CC to generate transgenic animals for use in development and screening of  
 CC therapeutically useful reagents and also for chromosome identification  
 CC and tissue typing.

XX Sequence 1712 BP; 491 A; 358 C; 388 G; 475 T; 0 other;

#### Alignment Scores:

| Pred. No.:             | 1.96e-99 | Length:       | 1712 |
|------------------------|----------|---------------|------|
| Score:                 | 1367.00  | Matches:      | 246  |
| Percent Similarity:    | 100.00%  | Conservative: | 0    |
| Best local Similarity: | 100.00%  | Mismatches:   | 0    |
| Query Match:           | 100.00%  | Indels:       | 0    |
| DB:                    | 21       | Gaps:         | 0    |

US-10-036-041-2 (1-246) x AAA96336 (1-1712)

OY 1 MetLeuTPaTgGlnLeuIleTyrTrpGlnLeuAlaLeuPhePheLeuProPheCys 20  
 DB 77 ATGCTTTGGAGGCACTATCTATTGGCACTCGGCTTTGTTTCTCCCTTTTTC 136  
 OY 21 LeuCySGlnAspGluTyrMetGluSerProGlnThrGlyLeuProProAspCysSer 40  
 DB 137 CTGTGTCAAGATGATATGATGAGTCTCCACAACCGAGGACTACCCGAGACTGAGT 196  
 OY 41 LysCySGlyHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60  
 DB 197 AAGTGTTCATGTGAGCTACAGCTTTCGAGGCTACCAAGGCCCCCTGGGGCCAGCGGC 256  
 OY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80  
 DB 257 CCTCTGGCATTTCCAGGAACCATGGAACATGGAACATGGAACCATGGAACATGGA 316  
 OY 81 GlyAlaTSGlyGluTyrGlyGlyAspGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGln 100  
 DB 317 GGAGCCAAAGGCGAAGGCGGCAAGGCTGACCTGGGGGCTCGAGGGGAGGGGGGCGAG 376  
 OY 101 HisGlyProGlyGlyGluGlyGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120  
 DB 377 CATGGCCCCAAGGAGAGAGGCGTACCCGGGATTCACCAAGAACTTCAGATTGCATTTC 436  
 OY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140  
 DB 437 ATGGCTTCTCTGGCAACCACTTCGCAATCAGAACATGGGATTAATCTTCAGCGAGTGT 496  
 OY 141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160  
 DB 497 GAGACCAACATTTGGAACCTCTTTGATGTCATGACTGGTAGATTGGGGGCCCACTATCA 556  
 OY 161 GlyValTyrPhePheThrPheSerMetMetGlyHisGlyAspValGluGluValTyrVal 180  
 DB 557 GGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGAGATGATATG 616  
 OY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetIleGlyHis 200  
 DB 617 TACCTTAATGCAATAGGACACACACTCTTCACATGTCACAGCTATGAATGAAGGGCAAA 676  
 OY 201 SerAspThrSerSerAsnHisAlaValLeuGlyLeuAlaGlyAspGluValTyrPhe 220  
 DB 677 TCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTGGCGT 736  
 OY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240  
 DB 737 CGAATGGGCAATGGGCGCTTCATGCGAGGAGCACCACCAACTCTCCACCTTCGAGGATTC 796  
 OY 241 LeuLeuPheGluThrHis 246  
 DB 797 CTGCTCTTTGAACACTAAG 814  
 RESULT 5  
 AAA95787  
 ID AAA95787 standard; cDNA; 1760 BP.  
 XX

AC AAA95787:  
 XX  
 DT 28-FEB-2001 (first entry)  
 DE  
 XX  
 DE Human immune system molecule cDNA from Incyte clone 1890540.  
 XX  
 KW Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianemic;  
 KW antiarteriosclerotic; antisthmatic; antidiabetic; nephroprotective; cancer;  
 KW immunosuppressive; cytostatic; fungicide; protozoacide; antibacterial;  
 KW gene therapy; diagnostic; immunological disorder; viral infection; ss;  
 KW bacterial infection; fungal infection; parasitic infection; immunogen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200060080-A2.  
 XX  
 PD 12-OCT-2000.  
 XX  
 PF 04-APR-2000; 2000WO-US09072.  
 XX  
 PR 05-APR-1999; 99US-0127852.  
 PR 05-MAY-1999; 99US-0132647.  
 XX  
 PA (INCYTE) INCYTE PHARM INC.  
 XX  
 PI Yue H, Lal P, Tang YT, Baughn MR, Azimzai Y, Lu DM;  
 XX  
 DR WPI: 2000-665005/64.  
 DR P-PSDB: AAB15548.  
 XX  
 PT New human immune system molecules 1-15 and polynucleotides encoding  
 PT them useful for diagnosing, treating or preventing e.g. immunological  
 PT disorders, infections, cell proliferative disorders, microbial  
 XX infections  
 XX  
 PS Claim 4; Page 93; 95pp: English.  
 XX  
 CC This sequence represents the cDNA for a human immune system molecule  
 CC (IMOL) isolated as clone 1890540 from the Incyte BLADrv07 library.  
 CC The human IMOLs (AAB15536-B15550) and their encoding polynucleotides  
 CC (AAA95775-A95789), and compositions comprising them are useful for the  
 CC diagnosis, treatment or prevention of immunological disorders,  
 CC infections and cell proliferative disorders, including cancer. The IMOL  
 CC may be used to treat or prevent disorders associated with decreased  
 CC expression or activity of IMOL, such as immunological disorders  
 CC (e.g. inflammation, actinic keratosis, AIDS, Addison's disease),  
 CC haematopoietic cancer, infections caused by virus (e.g. adenovirus,  
 CC parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus,  
 CC Shigella), fungi (e.g. Aspergillus, Blastomyces), parasites (e.g.  
 CC Plasmodium, Trypanosoma, intestinal protozoa), cell proliferative  
 CC disorders (e.g. actinic keratosis, arteriosclerosis, bursitis), and  
 CC cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also  
 CC useful as immunogens for the development of antibodies that  
 CC specifically recognizes these peptides. The polynucleotides may be used  
 CC to detect and quantify gene expression in biopsied tissues in which  
 CC expression of IMOL may be correlated with the disease, as targets in a  
 CC microarray, to detect differences in gene sequences among normal,  
 CC carrier and affected individuals, and for screening libraries of  
 CC compounds in drug screening techniques. Antibodies which specifically  
 CC bind to IMOL may be used for the diagnosis of disorders characterized  
 CC by expression of IMOL, or in assays to monitor patients being treated  
 CC with IMOL or agonists, antagonists, or inhibitors of IMOL.  
 CC  
 XX  
 SQ Sequence 1760 BP; 505 A; 376 C; 395 G; 484 T; 0 other;

#### Alignment Scores:

| Pred. No.:             | 2.02e-99 | Length:       | 1760 |
|------------------------|----------|---------------|------|
| Score:                 | 1367.00  | Matches:      | 246  |
| Percent Similarity:    | 100.00%  | Conservative: | 0    |
| Best local Similarity: | 100.00%  | Mismatches:   | 0    |
| Query Match:           | 100.00%  | Indels:       | 0    |
| DB:                    | 21       | Gaps:         | 0    |

US-10-036-041-2 (1-246) x AAA95787 (1-1760)

```
OY 1 MetLeuTTPaRGInLeuIleTyrrTPGInLeuAlaLeuPheLeuProPheCys 20
DB 124 ATGCTTTGGAGGAGCTCATCTATTTGGCAACTCTGCTTTGTTTCTCCCTTTTTC 183
OY 21 LeuCySGInAspGLuTyMeTGLuSerProGLaThrGLyGLyLeuProPAsPCysSer 40
DB 184 CTGTGTCAAGATGAATACATGAGAGTCTCCCAAAACCGGAGACTACCCCAAGACTG 243
OY 41 LysCySGySHISGLySPrySerPheArgLYTyrrGLInGLyProProGLyProProGLy 60
DB 244 AAGTGTTCATGAGAGACTACCTTTCGAGGCTACCAAGGCCCTTGCGCCACCGGGC 303
OY 61 ProProGLyIleProGLyAsnHISGLyAsnAsnGLyAsnAsnGLyAlaThrGLyHISGLu 80
DB 304 CCTCTGGCATTCACAGAAACCATGAAACAAATGCAACATGAGACCTGGTCATGAA 363
OY 81 GLyAlaLysGLyGLuTySGLyAspLysGLyAspLysGLyProArgGLyGLuArgGLyGLn 100
DB 364 GAGGCCAAAGGTAGAGAGGCGCAAAAGGTGACCTGGGCTTGAGGGGAGCGGGGAG 423
OY 101 HISGLyProLysGLyGLuTySGLyTyrrProGLyIleProProGLuLeuGLnIleAlaPhe 120
DB 424 CATGGCCCAAGAGAGAGAGGCTACCCGGGATTCACAGAACTTCAGATTGCAATTC 483
OY 121 MetAlaSerLeuAlaThrHISPheSerAsnGLInAsnSerGLyIleIlePheSerVal 140
DB 484 ATGGCTTCTGTGGCAACCCACTTCACCAATCAAGAAAGTGGATTATCTTCACACAGCTT 543
OY 141 GLuThrAsnIleGLyAsnPheAspValMetThrGLyArgPheGLyAlaProValSer 160
DB 544 GAGACCAACATTTGGAACCTCTTGTGATGCATACCTGTAAGATTGGGGCCCAAGATCA 603
OY 161 GLyValTyrrPhePheThrPheSerMetMetLysHISGLuAspValGLuGLuValTyrrVal 180
DB 604 GGGTGTATTCTTCTCACTTCAGCATGATGAAACATGAGATGTTGAGGAAGTATAGTG 663
OY 181 TyrrLeuMetHISAsnGLyAsnThrValPheSerMetTyrrSerTyrrGLuMetLysGLyLys 200
DB 664 TACCTTATGCACATGAGCAACAGTCTTCAGCATGTACAGCATGAATAAGAGGGCAAA 723
OY 201 SerAspThrSerSerAsnHISAlaValLeuLysLysLeuAlaLysGLyAspGLuValTyrrPleu 220
DB 724 TCAGATACATTCAGCAATCATGCTGTGCTGAGACCTAGCCAAAGGATGAGTTGGCTG 783
OY 221 ArgMetGLyAsnGLyAlaLeuHISGLyAspHISGLInArgPheSerThrPheAlaGLyPhe 240
DB 784 CGAATGGCAATGGCGCTCTCCATGGGAGCAACACGCTTTCACACTTTCAGAGATTTC 843
OY 241 LeuLeuPheGLuThrLys 246
DB 844 CTGCTCTTTGAAACTAAG 861

RESULT 6
ABK35590
ID ABK35590 standard; DNA; 960 BP.
XX
AC ABK35590;
XX
DT 08-MAY-2002 (first entry)
XX
DE Gene encoding novel human secreted or membrane-associated protein #9.
XX
KW Human; secreted protein; membrane-associated protein; hypertension;
KW inflammatory disorder; neurological disorder; haematopoietic disorder;
KW skeletal developmental disorder; growth abnormality; autoimmune disorder;
KW neurodegenerative disorder; nervous system disorder; bacterial infection;
KW peripheral myelinopathy; viral infection; cancer; obesity; diabetes;
KW hypotension; sexual development disorder; blood disorder; gene; ds.
XX
OS Homo sapiens.
```

```
XX
PN WO200204600-A2.
XX
PD 17-JAN-2002.
XX
PF 12-JUL-2001; 2001MO-US21985.
XX
PR 12-JUL-2000; 2000US-218033P.
PR 21-AUG-2000; 2000US-226517P.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PA (GLAX ) GLAXO GROUP LTD.
XX
PI Agarwal P, Cogswell JP, Lai Y, Martensen SA, Rizvi SK, Strum JC;
PI Smith RF, Xiang Z, Xie Q;
DR WPI: 2002-188468/24.
DR P-PSDB: AAU84370.
XX
PT Novel secreted and membrane-associated polypeptides and polynucleotides
PT encoding the polypeptides, for preventing, treating and ameliorating
PT cancers, mental or sexual developmental disorders, and malignant tumours
PT
XX
PS Claim 2; page 106; 151pp; English.
XX
CC The present invention relates to the isolation of novel human secreted
CC or membrane-associated proteins and the genes encoding them. The
CC sequences of the invention are useful for treating, preventing and
CC ameliorating various diseases such as inflammatory disorders (e.g.
CC asthma), neurological disorders (e.g. dementia), haematopoietic
CC disorders, skeletal developmental disorders, growth abnormalities,
CC neurodegenerative disorders (e.g. Huntington's disease), nervous system
CC disorders, autoimmune disorders (e.g. rheumatoid arthritis),
CC peripheral myelinopathies, viral and bacterial infections,
CC alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and
CC hypotension, obesity, bulimia, anorexia, manic depression, delirium,
CC mental retardation, Tourette's syndrome, schizophrenia, growth, mental
CC or sexual development disorders, and dysfunctions of the blood cascade
CC system including those leading to stroke. ABK35582-ABK35609 represent
CC the genes encoding the novel human secreted or membrane-associated
CC proteins of the invention.
XX
SO Sequence 960 BP; 261 A; 232 C; 262 G; 205 T; 0 other;

Alignment Scores:
Pred. No.: 4.94e-96 Length: 960
Score: 1320.50 Matches: 246
Percent Similarity: 77.128 Conservatve: 0
Best Local Similarity: 77.128 Mismatches: 0
Query Match: 96.608 Indels: 73
DB: 24 Gaps: 1

US-10-036-041-2 (1-246) x ABK35590 (1-960)
OY 1 MetLeuTTPaRGInLeuIleTyrrTPGInLeuAlaLeuPheLeuProPheCys 20
DB 1 ATGCTTTGGAGGAGCTCATCTATTTGGCAACTCTGCTTTGTTTCTCCCTTTTTC 60
OY 21 LeuCySGInAspGLuTyMeTGLuSerProGLaThrGLyGLyLeuProPAsPCysSer 28
DB 61 CTGTGTCAAGATGAATACATGAGAGTCTCCCAAAACCGGAGACTACCCCAAGACTG 120
OY 28 ----- 28
DB 121 GTGCAAGCAGCAGCAGAGACTGGCCCTACCGGCTCCAGAGAGGAGAGAAATGAGAGCGG 180
OY 28 ----- 28
DB 181 AGGCATCTAAAACTGGAGCTGTGATTAATACACTTTCACAGACCTAAATCCTGAGA 240
OY 28 ----- 28
```

|          |   |   |     |
|----------|---|---|-----|
| Db       | 241   | CCAAATGAGGCTACCGCACCCGAGGTAGATGACTTACCCAGATATCAACCATATCTGGGGC   | 300 |
| Qy       | 29  | ---SerProGlnThrGlyGlyLeuProProAspCysSerIscySHisGlyAspTyr        | 47  |
| Db       | 301   | CAGCTCCACAAACCGGAGGCTACCCCGACAGCTGAGTAAGTGTCTCATGGAGACTAC       | 360 |
| Qy       | 48  | SerPheArgGlyTyrGlnGlyProProGlyProProGlyProProGlyIleProGlyAsn    | 67  |
| Db       | 361   | AGCTTTGAGGCTTACCAAGGCCCCCTGGGCGCACCGGGCCCTCTGGCATTTCCAGGAAC     | 420 |
| Qy       | 68  | HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlyLeuAlaGlyGlyGlyGly       | 87  |
| Db       | 421   | CATGGAACAACATGGCACAACAATGAGGCCACTGGTCATGAGAGAGCAAGGTAAGAAGGC    | 480 |
| Qy       | 88  | AspIysGlyAspLeuGlyProArgGlyGlyLeuArgGlyGlnHisGlyProIlyGlyGlyLys | 107 |
| Db       | 481   | GACAAAGGTGACCTGGGGCCCTCGAGGGGAGCGGGGGCAGATGGCCCCAAAGAGAGAAC     | 540 |
| Qy       | 108   | GlyTyrProGlyIleProProGlyLeuGlnIleAlaPheMetAlaSerLeuAlaThrHis    | 127 |
| Db       | 541   | GGCTTACCGGGGATTTCCACGAACTTCACATTCATTCATGGCTTCTCTGGCAACCCAC      | 600 |
| Qy       | 128   | PheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhe    | 147 |
| Db       | 601   | TTTCAGCATTCAGAACAGTGGGATTTATCTTCAGCAGTGTTGAGACCAACATTGGAACTTC   | 660 |
| Qy       | 148   | PheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPhe    | 167 |
| Db       | 661   | TTTATATGACAGACTGGTAGATTTGGGGGCCCCAGCTATTCAGGTGTGTCTTCCACCTTC    | 720 |
| Qy       | 168   | SerMetMetLysHisGlyAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsn    | 187 |
| Db       | 721   | AGCATGATGAAGCATGAGAGATGTGAGGAATGTATGTGTACTTATGACCAATGGCAAC      | 780 |
| Qy       | 188   | ThrValPheSerMetTyrSerTyrGluMetLysGlyLysSerAspThrSerSerAsnHis    | 207 |
| Db       | 781   | ACAGCTCTTCACACATGATACAGCTATGAATAAGGCAAAATCAGATACATCAGCAATCAT    | 840 |
| Qy       | 208   | AlaValLeuLysLeuAlaIlyGlyAspGluValTyrLeuArgMetGlyAsnGlyAlaLeu    | 227 |
| Db       | 841   | GCTGCTGCGAAGCTAGGCCAAAGGGGATGAGGTTTGCTGCGAAATGGGCAATGGCGCTTC    | 900 |
| Qy       | 228   | HisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPheGluThrLys       | 246 |
| Db       | 901   | CATGGGAGCACCAACAGCTTCTCCACCTTTCAGAGATTCCGCTCTTTGAACATAAG        | 957 |
| RESULT 7 |   |   |     |
| AAC99776 |   |   |     |
| ID       | AAC99776  | standard; cDNA; 1035 BP.  |     |
| XX       | AAC99776;   |   |     |
| AC       |   |   |     |
| XX       | 08-MAR-2001 (first entry)   |   |     |
| DT       |   |   |     |
| XX       | Skin cell cDNA, SEQ ID NO: 424.                                     |   |     |
| DE       |   |   |     |
| XX       |   |   |     |
| KW       | Ret; skin cell; cyrostatic; antiinflammatory; anti-HIV;             |   |     |
| KW       | neurotropic; neuroprotective; vulnerary; immunomodulatory; vaccine; |   |     |
| KW       | keratinocyte growth stimulation; cancer; angiogenesis inhibition;   |   |     |
| KW       | inflammation; neurological disease; ss.                             |   |     |
| XX       |   |   |     |
| OS       | Rattus sp.  |   |     |
| XX       |   |   |     |
| PN       | W0200069884-h2.   |   |     |
| XX       |   |   |     |
| PD       | 23-NOV-2000.  |   |     |
| XX       |   |   |     |
| PF       | 15-MAY-2000; 2000WO-NZ00075.  |   |     |
| XX       |   |   |     |
| PR       | 14-MAY-1999; 99US-0312283.  |   |     |
| XX       |   |   |     |
| PA       | (GENE-) GENESIS RES & DEV CORP LTD.                                 |   |     |

|   |  |
|---|--|
| PI  | Watson JD, Strachan L, Onrust R, Sleeman M, Kumbie KD, Murison JG  |
| XX  |  |
| DR  | WPI: 2001-007495/01.   |
| XX  | P-PSDB: AAB55908.  |
| PT  | New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases -   |
| PS  | Claim 1; Page 317-318; 352pp; English.   |
| XX  |  |
| CC  | The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cell CC modulating angiogenesis, inhibiting angiogenesis and vascularisation o tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency vir CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and CC neurological diseases. The polynucleotide can be used as a marker, in CC the identification of genetic disorders, and for the design of oligonucleotides for examining expression patterns. |
| XX  |  |
| SQ  | Sequence 1035 BP; 255 A; 242 C; 298 G; 240 T; 0 other:   |
| Alignment Scores:                           |  |
| Pred. No.:                                  | 3,06e-95 Length: 1035  |
| Score:                                      | 1311.00 Matches: 236   |
| Percent Similarity:                         | 97.15% Conservative: 3   |
| Best Local Similarity:                      | 95.93% Mismatches: 7   |
| Query Match:                                | 95.908 Indels: 0   |
| DB:   | 22 Gaps: 0   |
| US-10-036-041-2 (1-246) x AAC99776 (1-1035) |  |
| OY  | 1 MetLeuPrpArgInLeuIleuIrrTrpGlnLeuLeuAlaLeuPheLeuProPhcys 20<br>            :   :   |
| Dd  | 92 ATGCTCAGAGGACGCCTCGTGGTGACACTGCTTCCTTTCTCCCATTTGC 151   |
| OY  | 21 LeucGslnaSpclutryMetGluSerProGlnThrGlyLeuProPaspCySer 40<br>  |
| Dd  | 152 CTGTGTAAGATGAATFCAATGAGATCTCCACAAGCTGGAGACTCCCCAAGCTGACG 211   |
| OY  | 41 LysGyScyShSglYasPyrSerPheaGlyTYrGlnGlyProProGlyProProgly 60<br>   |
| Dd  | 212 AAGGTGGCCATGAGATVTVGGATTCCGTGGTACCAGGGGCCCTGGACCCCACGT 271   |
| OY  | 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80<br>   |
| Dd  | 272 CTCCTCGCATTCAGGAAMCATGGAAMCATGGAATAAGAGAGCCACTGGCCACGAA 331  |
| OY  | 81 GlyAlaLysGlyLysGlyGlyAspLysGlyAspLeuGlyProArgGlyLunArgGlyGln 100<br>  |
| Dd  | 332 GGGGCCAAGGGTGAGAAAGGAGACAAAGGCGACTGGGCCCTCGAGGGGAAAGCGGGCAG 391  |
| OY  | 101 HisGlyProIlyGlyGlyLysGlyTYrTrpProGlyIleProProGlnLeuGlnIleAlaPhe 120<br>  |
| Dd  | 392 CATGGCCCCAAGGATAGAAGGATACCCAGGGGGTCCACACAGACTCCAGATTGCGTTC 451   |
| OY  | 121 MetLaserLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140<br>  |
| Dd  | 452 ATGGCTTCTAGGAGACTCACTTCAGACATACGAACAGGCGCATTTATCTTCAGCAGTGT 511  |
| OY  | 141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160<br>   |
| Dd  | 512 GAGACCAACATGGAAACTTCTTGATGTCATCACGTGATGATTTGGGCCCCCGTATCA 571  |
| OY  | 161 GlyAlaTyrrPhePheThrPheSerMetMetLysHisGlyAspValGlGlyValTyrrVal 180<br>  |
| Dd  | 572 GGCGTGTATTTCTTCACTTCACACATGATGAACATGAGAGACGTGGAGAAGTGATGTG 631   |
| OY  | 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200<br>   |

Db 632 TACCTTATGCACAAATGTTAAACACGGTGTTCAGCATGTACACTATGAAACAAGGAAAA 691  
Qy 201 SerapthrsersersasnhisalaValleuylsleualalySgIyAspGluValITrpleu 220  
Db 692 TCACATACATCCACCAACCAATGCTGAGTGGCCAAAGAGATGAGTGTGGCTA 751  
Qy 221 ArgmetGlyasnGlyAlaLeuHnIsgIyAspHisGlnArpHeserThrPheAlaGlyPhe 240  
Db 752 AGAATGGGCAACGGTGGCCCTTCATGGGACCAACGCGCTTCTTACCTTGGCAGGCTTT 811  
Qy 241 LeuLeupheGluThrLys 246  
Db 812 CTCCTTTTGAACCTAAG 829  
RESULT 8  
ABL34928  
ID ABL34928 standard; cDNA: 1035 BP.  
AC ABL34928;  
XX  
DT 04-APR-2002 (first entry)  
XX  
DE Rat cDNA isolated from skin cells SEQ ID NO: 424.  
XX  
KM Human; rat; mouse; skin cell; skin wound; cancer; growth defect;  
KM developmental defect; inflammatory disease; dermatological; vulnary;  
KM immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;  
KM ss.  
XX Rattus sp.  
OS  
XX MO200190357-A1.  
PN  
XX 29-NOV-2001.  
PD  
XX 24-MAY-2001; 2001MO-NZ00099.  
PF  
XX 24-MAY-2000; 2000US-20650P.  
PR 25-JUL-2000; 2000US-221232P.  
XX  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PI  
XX Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;  
XX WPI: 2002-122020/16.  
DR  
XX  
XX New polynucleotides and polypeptides encoded by the polynucleotides  
PT isolated from skin cells, useful for treating skin wounds, cancers,  
PT growth and developmental defects, inflammatory diseases, or for  
PT modulating immune responses  
XX  
XX Claim 1; Page 262; 466pp; English.  
XX  
XX The present invention provides the protein and coding sequences of cDNAs  
CC isolated from human, murine and rat skin cell libraries. The sequences  
CC can be used in the development of therapeutic agents useful in the  
CC treatment of skin diseases, including skin wounds, cancer, growth  
CC defects, developmental defects and inflammatory diseases. The proteins  
CC have important roles in the induction of hair growth, cell proliferation  
CC and cell-cell interaction, in maintaining tissue integrity, in wound  
CC healing and in modulating immune responses. The present sequence is a  
CC cDNA of the invention.  
XX  
XX Sequence 1035 BP; 255 A; 242 C; 298 G; 240 T; 0 other;  
XX  
XX  
XX Alignment Scores:  
Pred. No.: 3 06e-95 Length: 1035  
Score: 1311.00 Matches: 236  
Percent Similarity: 97.15% Conservative: 3  
Best Local Similarity: 95.93% Mismatches: 7  
Query Match: 95.90% Indels: 0  
DB: 24 Gaps: 0

US-10-036-041-2 (1-246) x ABL34928 (1-1035)  
Qy 1 MetleuTrpArgGlnLeuIleTyrTrpGlnLeuAlaLeuPhePheLeuProPheCys 20  
Db 92 ATGCTTACAG 151  
Qy 21 LeuCysGlnAspGluTyrMetGlnSerProGlnHnIsgIyLysLeuProAspCysSer 40  
Db 152 CTGCTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 211  
Qy 41 LysCysCysHnIsgIyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60  
Db 212 AAGTGTTCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 271  
Qy 61 ProProGlyIleProGlyAsnHnIsgIyAsnAsnGlnAsnGlnAlaThrGlyHnIsgIu 80  
Db 272 CTCCTGCGATTCAG 331  
Qy 81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLysGlyProArgGlyGlnArgGlyGln 100  
Db 332 GGGGCCAAGGGTGAAGAAAGAGAACAAAGGCGACCTGGGGCTCGAGGGGAAGGGGGCAG 391  
Qy 101 HnIsgIyProLysGlyLysGlyLysGlyTyrProGlyIleProProGlyLysGlnIleAlaPhe 120  
Db 392 CATGGCCCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 451  
Qy 121 MetAlaSerLeuAlaThrHnIspHeserAsnGlnAsnSerGlyIleIlePheSerSerVal 140  
Db 452 ATGCTTCTCTAGGAGACCTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 511  
Qy 141 GluThrAsnIleGlyAsnPhaPheAspValMetTrpGlyArgPheGlyAlaProValSer 160  
Db 512 GAGACCAACATTTGAAACTTCTTCATGTGATGATGATGATGATGATGATGATGATGATGAT 571  
Qy 161 GlyAlaTyrPhePheThrPheSerMetMetLysHnIsgIyAspValGluGlyValTyrVal 180  
Db 572 GCGGTGATTTCTTCACCTTCAGCATGATGATGATGATGATGATGATGATGATGATGATGAT 631  
Qy 181 TyrLeuMetHnIsgIyAsnThrValPheSerMetTyrSerTyrGlyMetLysGlyLys 200  
Db 632 TACCTTATGCACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691  
Qy 201 SerapthrsersersasnhisalaValleuylsleualalySgIyAspGluValITrpleu 220  
Db 692 TCACATACATCCACCAACCAATGCTGAGTGGCCAAAGAGATGAGTGTGGCTA 751  
Qy 221 ArgmetGlyasnGlyAlaLeuHnIsgIyAspHisGlnArpHeserThrPheAlaGlyPhe 240  
Db 752 AGAATGGGCAACGGTGGCCCTTCATGGGACCAACGCGCTTCTTACCTTGGCAGGCTTT 811  
Qy 241 LeuLeupheGluThrLys 246  
Db 812 CTCCTTTTGAACCTAAG 829  
RESULT 9  
AAC64064  
ID AAC64064 standard; DNA: 1117 BP.  
XX  
XX AAC64064;  
AC  
XX 19-FEB-2001 (first entry)  
DT  
XX  
XX Mouse zacr2p2 DNA, SEQ ID NO:11.  
DE  
XX  
XX Mouse zacr2p2; adipocyte complement related protein homologue;  
KM ACRP30; C1q domain; collagen-like domain; energy balance modulation;  
KM cellular metabolism; metabolic disorder; obesity; anorexia;  
KM antimicrobial agent; infection; platelet aggregation inhibition;  
KM adhesion; activation; vascular injury; antibacterial; antiviral;  
KM human zacr2p2 homologue; ds.  
XX  
XX Mus musculus.







PS Claim 1; Page 73; 235pp; English.

XX The invention relates to novel nucleic acid sequences derived from rat

CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,

CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying

CC cells. Polypeptides of the invention may be used to treat inflammation,

CC cancer and neurological diseases. The proteins may be used to stimulate

CC the growth and motility of keratinocytes, to inhibit the growth of

CC cancer cells, to modulate angiogenesis and tumour vascularisation, to

CC modulate skin inflammation, to modulate epithelial cell growth and to

CC inhibit binding of HIV-1 to leukocytes. The invention may also be used

CC to treat growth and developmental defects, skin wounds and hair follicle

CC disorders. Sequences AA261606-261817 represent cDNA sequences derived

CC from several mouse, rat or human skin cell types. Sequences

CC AA261606-261649, AA261725-261765, AA261802-261811 and AA261826 encode

CC proteins with an N-terminal signal sequence, indicating that the proteins

CC are secreted. Sequences AA261650-261668, AA261766-261780, AA261812-261817

CC and AA261827-261829 encode proteins with one or more putative

CC transmembrane domains.

CC XX

SQ Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

Alignment Scores:

| Pred. No.:             | 3,36e-95 | Length:       | 1123 |
|------------------------|----------|---------------|------|
| Score:                 | 1311.00  | Matches:      | 236  |
| Percent Similarity:    | 97.15%   | Conservative: | 3    |
| Best Local Similarity: | 95.93%   | Mismatches:   | 7    |
| Query Match:           | 95.90%   | Indels:       | 0    |
| DB:                    | 21       | Gaps:         | 0    |

US-10-036-041-2 (1-246) x AA261633 (1-1123)

OY 1 MetLeuTrpArgGlnLeuIleTyTTPGlnLeuAlaLeuPheLeuProPheCys 20

DB 180 ATGCTCAGGAGGCGAGCTCGTGTGGCACCCTGCTTGTCTTCTCCATTTTGC 239

OY 21 LeuCysGlnAspGluTyTMetGluSerProGlnThrGlyLeuProProAspCysSer 40

DB 240 CTGTGTCAAGTCAATCATGAGACTCTCCACACCTGAGAGAGCCGCCACAGATGAGC 299

OY 41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProGly 60

DB 300 AAGTGTGCCATGAGATTATGATTCGCGTGTACCAAGGCGCCCTTGAGCCGCCAGGT 359

OY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80

DB 360 CCTCTGCGCATTCACGAAACCATGAAACAATGAAATTAACGAGGACCTGCGCACGAA 419

OY 81 GlyAlaLysGlyGlyLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100

DB 420 GGGGCCCAAGGGGTGAGAAAGAGACAAAGCGACCTGGGGCTCGAGGGGCAACGGGGCAG 479

OY 101 HisGlyProLysGlyGlyLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120

DB 480 CATGGCCCCAAGATGAAAGGAGATACCCAGGGGTGCCACCAAGCTGCAGATTGCCCTTC 539

OY 121 MetaLaserLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerVal 140

DB 540 ATGGCTTCTAGAGCACTCACTCAGCAATCAGAACAGTGCATTATCTTCAGACAGTGT 599

OY 141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160

DB 600 GAGAGCAACATTTGAAACTTCTTCGATGTCATGCTGTGATTGGGGCCCCCGTATCA 659

OY 161 GlyValTyrPhePheThrPheSerMetCysHisGlyAspValGluGluValTyrVal 180

DB 660 GCGCTGATTTCTTCACCTTCAGCATATGACATAGACAGCGGAGGAAGTATAGTG 719

OY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200

DB 720 TACCTTATGCAACATGATGTAACACGCTGTCAGCATGTACAAACAAAGGAGAAA 779

OY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTTPleu 220

DB 780 TCAGATACATCCACACACATGCTGTAAGTTGGCCAAAGAGATGAATCTGGCTA 839

OY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240

DB 840 AGAATGGGCAACGGTGGCCCTCATGGGACACACAGCCCTTCTACATTTGGCAGCTTT 899

OY 241 LeuLeuPheGluThrLys 246

DB 900 CTGCTTTTGAACCTAAG 917

RESULT 11

AA261730

ID AA261730 standard; cDNA: 1123 BP.

XX

AC AA261730;

XX

DT 27-MAR-2000 (first entry)

XX

DE cDNA encoding rat skin cell secreted protein, SEQ ID NO:203.

XX

XX Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;

KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell;

KW secreted; transmembrane; inflammation; cancer; neurological disease;

KW angiogenesis; tumour vascularisation; growth disorder;

KW developmental disorder; skin wound; hair follicle disorder;

KW anti-inflammatory; cytostatic; neuroprotective; vulnery; ss.

OS Ratus sp.

XX

PN MO9955865-A1.

XX

PD 04-NOV-1999.

XX

PF 29-APR-1999; 99MO-NZ00051.

XX

PR 29-APR-1998; 98US-0069726.

PR 09-NOV-1998; 98US-0188930.

XX

PA (GENE-) GENESIS RES & DEV CORP LTD.

PI Strachan L, Sleeman M, Watson JD, Omrust R, Kumble A, Murison JG;

DR P-PSDB: AAY76025.

XX

PT Novel polynucleotides useful for the treatment of various conditions

XX including wounds and cancer -

PS Claim 1; Page 137; 235pp; English.

XX

CC The invention relates to novel nucleic acid sequences derived from rat

CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,

CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying

CC cells. Polypeptides of the invention may be used to treat inflammation,

CC cancer and neurological diseases. The proteins may be used to stimulate

CC the growth and motility of keratinocytes, to inhibit the growth of

CC cancer cells, to modulate angiogenesis and tumour vascularisation, to

CC modulate skin inflammation, to modulate epithelial cell growth and to

CC inhibit binding of HIV-1 to leukocytes. The invention may also be used

CC to treat growth and developmental defects, skin wounds and hair follicle

CC disorders. Sequences AA261606-261817 represent cDNA sequences derived

CC from several mouse, rat or human skin cell types. Sequences

CC AA261606-261649, AA261725-261765, AA261802-261811 and AA261826 encode

CC proteins with an N-terminal signal sequence, indicating that the proteins

CC are secreted. Sequences AA261650-261668, AA261766-261780, AA261812-261817

CC and AA261827-261829 encode proteins with one or more putative

CC transmembrane domains.

CC XX

SQ Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

Alignment Scores:

| Pred. No.: | 3,36e-95 | Length: | 1123 |
|------------|----------|---------|------|
|------------|----------|---------|------|



|||||  
Db 540 ATGGCTTCTTACGAGCTCTCAGCAATCAACAGTGGCTTATCTTACAGAGTGT 539  
QY 141 GluThrAsnIleGlyAsnPhenPheAspValMetThrGlyArgPheGlyAlaProValSer 160  
Db 600 GAGACCAACATGTGAAGACTCTTCGATGTCATGATGATGATGGGGCCCCCATCA 659  
QY 161 GlyValTyrPhePhePhePheSerMetMetLysHisGluAspValGluGluValTyrVal 180  
Db 660 GGGGTGATTTCTTCACTTCACATGATGATGATGATGATGATGATGATGATGATG 719  
QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200  
Db 720 TACCTTATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 779  
QY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPleu 220  
Db 780 TCAGATGATCATGCAACCATGATGATGATGATGATGATGATGATGATGATGATG 839  
QY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240  
Db 840 AGATGGGCAACGGTCCCTCCATGGGAGACACAGCGCTTCTCTACCTTCGACGCTTT 899  
QY 241 LeuLeuPheGluThrLys 246  
Db 900 CTCCTTTTGAACCTAAG 917  
RESULT 13  
AAC99663  
ID AAC99663 standard; cDNA; 1123 BP.  
XX  
AC AAC99663;  
XX  
DT 08-MAR-2001 (first entry)  
XX  
DE Skin cell cDNA, SEQ ID NO: 203.  
XX  
XX Rat; skin cell; cytostatic; antiinflammatory; anti-HIV;  
KW neutropic; neuroprotective; vulnerrary; immunomodulatory; vaccine;  
KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;  
KW inflammation; neurological disease; ss.  
XX  
OS Rattus sp.  
XX  
XX WO200069884-A2.  
XX  
PD 23-NOV-2000.  
XX  
PF 15-MAY-2000; 2000MO-NZ00075.  
XX  
PR 14-MAY-1999; 99US-0312283.  
XX  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
XX  
PI Watson JD, Strachan L, Orust R, Sleeman M, Kumble KD, Murison JG;  
DR WPI; 2001-007495/01.  
DR P-PSDB; AAB55958.  
XX  
XX New isolated polynucleotide used in the identification of genetic  
PT disorders and encoding polypeptides used for treating inflammatory  
PT disease, cancer and neurological diseases -  
XX  
XX Claim 1; Page 176-177; 352p; English.  
XX  
XX The present polynucleotide encodes a polypeptide which is expressed in  
CC mammalian skin cells. The polypeptide is useful for stimulating  
CC keratinocyte growth and motility, inhibiting the growth of cancer cells,  
CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of  
CC tumours, modulating skin inflammation, stimulating the growth of  
CC epithelial cells, inhibiting the binding of human immunodeficiency virus  
CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and  
CC neurological diseases. The polynucleotide can be used as a marker, in

CC the identification of genetic disorders, and for the design of  
CC oligonucleotides for examining expression patterns.  
XX  
SQ Sequence 1123 BP: 277 A; 266 C; 321 G; 258 T; 1 other;  
Alignment Scores:  
Pred. No.: 3 36e-95  
Score: 1311.00  
Percent Similarity: 97.15%  
Best Local Similarity: 95.93%  
Query Match: 95.90%  
DB: 22  
Gaps: 0  
US-10-036-041-2 (1-246) x AAC99663 (1-1123)  
QY 1 MetLeuTrrPargInleuLleTrrTrrGlnLeuLeuAlaLeuPheLeuPropheCys 20  
Db 180 ATGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 239  
QY 21 LeuGlyGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40  
Db 240 CTGTGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 299  
QY 41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60  
Db 300 AAGTGTTCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 359  
QY 61 ProProGlyLleProGlyAsnHisGlyAsnGlyAsnGlyAsnGlyAlaThrGlyHisGlu 80  
Db 360 CCTCCGCGCATTCACAGAAACCATGCAACATGCAACATGCAACATGCAACATG 419  
QY 81 GlyAlaLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 100  
Db 420 GGGGCCAAGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 479  
QY 101 HisGlyProLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 120  
Db 480 CATGGCCCCCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 539  
QY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyLleLeuPheSerSerVal 140  
Db 540 ATGCTTCTTACGAGCTCACTCAGCAATCAGACAGAGTGTATTCACACAGTGT 599  
QY 141 GluThrAsnIleGlyAsnPhenPheAspValMetThrGlyArgPheGlyAlaProValSer 160  
Db 600 GAGACCAACATGTGAAGACTCTTCGATGTCATGATGATGATGATGATGATGATG 659  
QY 161 GlyValTyrPhePhePhePheSerMetMetLysHisGluAspValGluGluValTyrVal 180  
Db 660 GGGGTGATTTCTTCACTTCACATGATGATGATGATGATGATGATGATGATGATG 719  
QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200  
Db 720 TACCTTATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 779  
QY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPleu 220  
Db 780 TCAGATGATCATGCAACCATGATGATGATGATGATGATGATGATGATGATGATG 839  
QY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240  
Db 840 AGATGGGCAACGGTCCCTCCATGGGAGACACAGCGCTTCTCTACCTTCGACGCTTT 899  
QY 241 LeuLeuPheGluThrLys 246  
Db 900 CTCCTTTTGAACCTAAG 917  
RESULT 14  
ABL34718  
ID ABL34718 standard; cDNA; 1123 BP.  
XX  
XX ABL34718;  
XX

|   |  |
|---|--|
| DT  | 04-APR-2002 (first entry)  |
| XX  |  |
| DE  | Rat cDNA isolated from skin cells SEQ ID NO: 28.                         |
| XX  |  |
| XX  | Human; rat; mouse; skin cell; skin wound; cancer; growth defect;         |
| KW  | developmental defect; inflammatory disease; dermatological; vulnary;     |
| KM  | immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;   |
| XX  | ss.  |
| OS  | Rattus sp.   |
| XX  |  |
| PX  | WO200190357-A1.  |
| XX  |  |
| PD  | 29-NOV-2001.   |
| PF  | 24-MAY-2001; 2001WO-NZ00099.   |
| PR  | 24-MAY-2000; 2000US-206650P.   |
| PR  | 25-JUL-2000; 2000US-221232P.   |
| PA  | (GENE-) GENESIS RES & DEV CORP LTD.                                      |
| PI  | Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD,       |
| DR  | WPI: 2002-122020/16.   |
| XX  |  |
| PT  | New polynucleotides and polypeptides encoded by the polynucleotides      |
| PT  | isolated from skin cells, useful for treating skin wounds, cancers,      |
| PT  | growth and developmental defects, inflammatory diseases, or for          |
| PT  | modulating immune responses -  |
| XX  |  |
| PS  | Claim 1; Page 86-87; 466pp: English.                                     |
| CC  |  |
| CC  | The present invention provides the protein and coding sequences of cDNAs |
| CC  | isolated from human, murine and rat skin cell libraries. The sequences   |
| CC  | can be used in the development of therapeutic agents useful in the       |
| CC  | treatment of skin diseases, including skin wounds, cancer, growth        |
| CC  | defects, developmental defects and inflammatory diseases. The proteins   |
| CC  | have important roles in the induction of hair growth, cell proliferation |
| CC  | and cell-cell interaction, in maintaining tissue integrity, in wound     |
| CC  | healing and in modulating immune responses. The present sequence is a    |
| CC  | cDNA of the invention.   |
| XX  |  |
| XQ  | Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other:                   |
| Alignment Scores:                           |  |
| Pred. No.:                                  | 3 36e-95 Length: 1123  |
| Score:                                      | 1311.00 Matches: 236   |
| Percent Similarity:                         | 97.15% Conservative: 3   |
| Best Local Similarity:                      | 95.93% Mismatches: 7   |
| Query Match:                                | 95.90% Indels: 0   |
| DB:   | 24 Gaps: 0.  |
| US-10-036-041-2 (1-246) x ABL34718 (1-1123) |  |
| OY  | 1 MetLeuTPAAGAGlnLeuIleTYTfPGlInDeulaIaIeuPhenheUeuProPhCys 20           |
| Dd  | 180 ATGCCTACAGAGCAAGCGTCGTGGTGGCACCTGCTGGCTTTGCCATTTTG 239               |
| OY  | 21 LeucySGlnAspGlyTYrMetGIserPProGlnThrlgLyLeuProProAsCySser 40          |
| Dd  | 240 CTGTGTCAAGATGAATCATGTGACTCCACAACTGGAGAGACTGCCCCAGACTGACG 299         |
| OY  | 41 LysCYSCYSNHISGLYASPTYSerPhaargLYyrTrInglYrProProGlyrProProGly 60      |
| Dd  | 300 AAGTGTTCCTCCATGGAGATTATGATTCGCTGTTCACCAAGGGCCCCCTGACCCCAGGT 359      |
| OY  | 61 ProProGlyILIEProGlyAsnHISGLYAsnaSnGLYasnaSnGLYalaThrGlyNHISGL 80      |
| Dd  | 360 CCTCTGGCATTTCCAGGAACAACATGGAATAACGAGGACCTGGCCACGAA 419               |
| OY  | 81 GlyAlaLysGLYGLYLysGLYAsPLysGLYAsPLeuGLYProArGLYGLYuarGLYGLn 100       |

|           |   |  |     |
|-----------|---|--|-----|
| Db        | 420   | GGGGCCAGGGGTGCAGAAAGACACAAAGCGACCTGGGGCCCTCGAGGGGACAGCGGGGCGAG | 479 |
| Qy        | 101   | HisGlyProLysGlyLysGlyTyrProGlyIleProGlyIleuGlnIleAlaPhe        | 120 |
| Db        | 480   | CATGGGCCCCAAGATAGAAAGGATATCCACAGGGGTCCACACAGACTGCAGATTGGCTTC   | 539 |
| Qy        | 121   | MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerVal      | 140 |
| Db        | 540   | ATGGCTTCCTAGCCACTCACTTCACCAATCAGAACAGTGGGATATATCTTCAGCACTGTT   | 599 |
| Qy        | 141   | GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer   | 160 |
| Db        | 600   | GGAGCCACATTTGGAAACTTCTTCATGATCACTGATGATTTGGGCCCCCGATATA        | 659 |
| Qy        | 161   | GlyValTyrPhePheThrPheSerMetMetLysHisGlyAspValGluGlyValTyrVal   | 180 |
| Db        | 660   | GGCGGTATTCTTCTACCTTCACGATGATGAAGCATGAGAGCTGGAGAAAGTATGTG       | 719 |
| Qy        | 181   | TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys   | 200 |
| Db        | 720   | TACCTTATCCAAATGTGTAAACAGCGGTCTCAGCATGTACAGCATATGAACAAAGGAGAAA  | 779 |
| Qy        | 201   | SerAspThrSerSerAsnHisAlaValLeuLysIleuAlaLysGlyAspGluValTyrLeu  | 220 |
| Db        | 780   | TGAGATACATTCACGACACCATCGATGCTGAAGTTGGCCAAAGAGATGAATCTGGCTTA    | 839 |
| Qy        | 221   | ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe   | 240 |
| Db        | 840   | ACAAATGGGACAGCGTCCCTCCATGGGGGACACACAGCGCTTCTCTACCTTCGACGCTTT   | 899 |
| Qy        | 241   | LeuLeuPheGluThrLys 246   |     |
| Db        | 900   | CTGCTTTTGAACATGAG 917  |     |
| RESULT 15 |   |  |     |
| ABL34815  |   |  |     |
| ID        | ABL34815  | standard; cDNA; 1123 BP.                                       |     |
| AC        | ABL34815;   |  |     |
| XX        |   |  |     |
| DT        | 04-APR-2002   | (first entry)  |     |
| XX        |   |  |     |
| DE        | Rat cDNA isolated from skin cells                                     | SEQ ID NO: 203.  |     |
| XX        |   |  |     |
| KM        | Human; rat; mouse; skin cell; skin wound; cancer; growth defect;      |  |     |
| KM        | developmental defect; inflammatory disease; dermatological; vulneray; |  |     |
| KM        | immunomodulator; anti-inflammatory; cytosatic; neuroprotective; gene; |  |     |
| KM        | ss.   |  |     |
| XX        |   |  |     |
| OS        | Rattus sp.  |  |     |
| XX        |   |  |     |
| PN        | WO200190357-A1.   |  |     |
| XX        |   |  |     |
| PD        | 29-NOV-2001.  |  |     |
| XX        |   |  |     |
| PF        | 24-MAY-2001; 2001WO-NZ00099.  |  |     |
| XX        |   |  |     |
| PR        | 24-MAY-2000; 2000US-206650P.  |  |     |
| PR        | 25-JUL-2000; 2000US-22132P.   |  |     |
| XX        |   |  |     |
| PA        | (GENE-) GENESIS RES & DEV CORP LTD.                                   |  |     |
| PI        | Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD,    |  |     |
| DR        | WPI; 2002-122020/16.  |  |     |
| XX        |   |  |     |
| XX        | New polynucleotides and polypeptides encoded by the polynucleotides   |  |     |
| PT        | isolated from skin cells, useful for treating skin wounds, cancers,   |  |     |
| PT        | growth and developmental defects, inflammatory diseases, or for       |  |     |
| XX        | modulating immune responses   |  |     |
| PS        | Claim 1; Page 155-156; 466pp; English.                                |  |     |
| XX        |   |  |     |



| Result No. | Score | Query Match | Length | DB | ID                | Description        |
|------------|-------|-------------|--------|----|-------------------|--------------------|
| 1          | 1311  | 95.9        | 1123   | 3  | US-09-188-930-28  | Sequence 28, Appl  |
| 2          | 1311  | 95.9        | 1123   | 3  | US-09-188-930-203 | Sequence 203, Appl |
| 3          | 316   | 23.1        | 1107   | 3  | US-09-188-930-217 | Sequence 217, Appl |
| 4          | 299   | 21.9        | 1276   | 3  | US-08-463-911-1   | Sequence 1, Appl   |
| 5          | 293.5 | 21.5        | 1313   | 2  | US-08-463-911-6   | Sequence 6, Appl   |
| 6          | 293.5 | 21.5        | 4517   | 4  | US-09-140-804-9   | Sequence 9, Appl   |
| 7          | 273   | 20.0        | 3275   | 4  | US-09-370-838-151 | Sequence 151, Appl |
| 8          | 264.5 | 19.3        | 1333   | 4  | US-09-527-357-51  | Sequence 51, Appl  |
| 9          | 264.5 | 19.3        | 1343   | 4  | US-09-140-804-1   | Sequence 1, Appl   |
| 10         | 257   | 18.8        | 729    | 4  | US-09-336-536-9   | Sequence 9, Appl   |
| 11         | 257   | 18.8        | 1263   | 4  | US-09-336-536-8   | Sequence 8, Appl   |
| 12         | 254.5 | 18.6        | 1015   | 3  | US-09-188-930-30  | Sequence 30, Appl  |

|    |       |      |       |   |                    |                    |
|----|-------|------|-------|---|--------------------|--------------------|
| 13 | 252.5 | 18.5 | 1001  | 3 | US-09-188-930-218  | Sequence 218, App  |
| 14 | 251   | 18.4 | 728   | 4 | US-09-336-536-2    | Sequence 2, App1   |
| 15 | 251   | 18.4 | 1338  | 4 | US-09-336-536-1    | Sequence 1, App1   |
| 16 | 241   | 17.6 | 1839  | 1 | US-08-383-744-1    | Sequence 1, App1   |
| 17 | 241   | 17.6 | 1839  | 2 | US-08-999-336-1    | Sequence 1, App1   |
| 18 | 241   | 17.6 | 1839  | 5 | PCT-US96-01427-1   | Sequence 1, App1   |
| 19 | 237.5 | 17.4 | 2559  | 4 | US-09-118-408-43   | Sequence 43, App1  |
| 20 | 237.5 | 17.4 | 2559  | 4 | US-09-506-855-43   | Sequence 43, App1  |
| 21 | 226   | 16.5 | 2769  | 4 | US-09-118-408-1    | Sequence 1, App1   |
| 22 | 226   | 16.5 | 2769  | 4 | US-09-506-855-1    | Sequence 1, App1   |
| 23 | 216.5 | 15.8 | 729   | 4 | US-09-140-804-10   | Sequence 10, App1  |
| 24 | 203.5 | 14.9 | 4359  | 4 | US-09-484-970B-4   | Sequence 4, App1   |
| 25 | 200.5 | 14.7 | 750   | 3 | US-08-188-930-19   | Sequence 19, App1  |
| 26 | 195.5 | 14.3 | 4031  | 1 | US-08-159-768-1    | Sequence 1, App1   |
| 27 | 192   | 14.0 | 1881  | 4 | US-09-029-348-20   | Sequence 20, App1  |
| 28 | 191   | 14.0 | 983   | 4 | US-09-247-155-153  | Sequence 153, App1 |
| 29 | 189   | 13.8 | 653   | 4 | US-09-336-536-32   | Sequence 32, App1  |
| 30 | 187   | 13.7 | 3394  | 1 | US-08-159-768-4    | Sequence 1, App1   |
| 31 | 185   | 13.5 | 48908 | 4 | US-09-453-702B-137 | Sequence 137, App1 |
| 32 | 184.5 | 13.5 | 2543  | 1 | US-08-073-668-11   | Sequence 11, App1  |
| 33 | 184.5 | 13.5 | 2543  | 3 | US-09-073-668-11   | Sequence 11, App1  |
| 34 | 184   | 13.5 | 3404  | 4 | US-09-453-702B-54  | Sequence 94, App1  |
| 35 | 183   | 13.4 | 1868  | 1 | US-08-392-367B-1   | Sequence 1, App1   |
| 36 | 183   | 13.4 | 1868  | 3 | US-08-893-4376A-1  | Sequence 1, App1   |
| 37 | 182   | 13.3 | 1560  | 2 | US-08-794-795-5    | Sequence 5, App1   |
| 38 | 182   | 13.3 | 1560  | 4 | US-09-249-200-5    | Sequence 5, App1   |
| 39 | 182   | 13.3 | 1703  | 2 | US-08-794-795-1    | Sequence 1, App1   |
| 40 | 182   | 13.3 | 1703  | 4 | US-09-249-200-1    | Sequence 1, App1   |
| 41 | 179.5 | 13.1 | 1560  | 4 | US-09-453-702B-64  | Sequence 64, App1  |
| 42 | 179.5 | 13.1 | 61663 | 4 | US-09-453-702B-62  | Sequence 62, App1  |
| 43 | 179   | 13.1 | 186   | 1 | US-07-609-716-62   | Sequence 62, App1  |
| 44 | 179   | 13.1 | 186   | 1 | US-08-642-255-30   | Sequence 30, App1  |
| 45 | 179   | 13.1 | 186   | 3 | US-08-473-411A-62  | Sequence 62, App1  |

## ALIGNMENTS

## RESULT 1

```

US-09-188-930-28
? Sequence 28, Application US/09188930A
? Patent No. 6150502
? GENERAL INFORMATION:
? APPLICANT: Watson, James D.
? APPLICANT: Strachan, Lorna
? APPLICANT: Sleeman, Matthew
? APPLICANT: Onrust, Rene
? APPLICANT: Murison, James Greg
? TITLE OF INVENTION: Compositions Isolated From Skin Cells
? TITLE OF INVENTION: and Methods For Their Use
? FILE REFERENCE: 11000.1011c1
? CURRENT APPLICATION NUMBER: US/09/188,930A
? CURRENT FILING DATE: 1998-11-09
? NUMBER OF SEQ ID NOS: 348
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 28
? LENGTH: 1123
? TYPE: DNA
? ORGANISM: Rat
US-09-188-930-28

```

### Alignment Scores:

|                        |           |               |     |
|------------------------|-----------|---------------|-----|
| Pred. No.:             | 1,2le-117 | Length:       | 112 |
| Score:                 | 1311.00   | Matches:      | 236 |
| Percent Similarity:    | 97.13%    | Conservative: | 3   |
| Best Local Similarity: | 95.93%    | Mismatches:   | 7   |
| Query Match:           | 95.90%    | Indels:       | 0   |
| DB:                    | 3         | Gaps:         | 0   |

US-10-036-041-2 (1-246) x US-09-188-930-28 (1-1123)

Oy 1 MetLeuTrpArgGlnLeuIleTyrTrpClnLeuAlaPhePheLeuProPheCys 20  
||||| |||||:::||| ||||| ||||| ||||| |||||  
Db 180 ATGTCAGAGGACAGCTCGTCGTGGCACACTGCTGGCTTTTCCTCCATTTC 23

```

QY 21 LeuCySGlnAspGluTyrMetGluSerProGlnThrGlyLeuProAspCysSer 40
    |||||
Db 240 CTGTCTCAAGATGAAATACATGAGTCTCCACAAGCTGAGAGACTGCCCCAGACTGCAGC 299
QY 41 LysCysCySHisGlySprSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
    |||||
Db 300 AAGTGTTCATGAGATGATGATTCCTGCTGTTACCAAGGCGCCCTTGAGCCCAAGGT 359
QY 61 ProProGlyIleProGlyLysnHisGlyAsnAsnGlyLysnAsnGlyAlaThrGlyHisGlu 80
    |||||
Db 360 CCGCTCGGATTCAGAGAAACCTGGAACAATGGAATACGAGAGCCACTGGCCAGAA 419
QY 81 GlyAlaLysGlyGlyLysGlyAspLysGlyAspLeuGlyProArgGlyLysGlyGln 100
    |||||
Db 420 GGGGCCCAAGGTCAGAAAGAGACAAAGGCGACCTGGGCGCTGAGGGGGAAGCGGGCAG 479
QY 101 HisGlyProLysGlyLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120
    |||||
Db 480 CATTGGCCCAAGGATGAGAGATACCCAGGGGGTGCACAGAGCTGCAGATTGGCTTC 539
QY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
    |||||
Db 540 ATGGCTTCTCTACCGACTCACTTACAGCAATCAGAACAGTGGCATTTATCTTCAGCAGTGT 599
QY 141 GluThrAsnIleGlyAsnPheAspValMetThrGlyArgPheGlyAlaProValSer 160
    |||||
Db 600 GAGACCAACATTGGAACACTCTTCGATGTCATGATGATGATTTGGGCGCCCGTATCA 659
QY 161 GlyValTyrPhePheThrPheSerMetMetLysHisGlyAspValGluGluValTyrVal 180
    |||||
Db 660 GCGGTGTATTTCTTCACCTTCACCATGATGAAATGAGACCTGAGAGAGTATGTTG 719
QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetLysSerTyrGlnMetLysGlyLys 200
    |||||
Db 720 TACCTTATGACACATGTAACACGAGTGTTCAGCATGTACAGCTATGAAACAAAGGAGAAA 779
QY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPleu 220
    |||||
Db 780 TCAGATACATCCAGCAACCATGAGTGCATGAACTGGCCAAAGAGATGATGCTG 839
QY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
    |||||
Db 840 AGAATGGCAAGCGTCCCTCCATGGGAGCCACAGCGCTTCTCTACCTTCGACGCTTT 899
QY 241 LeuLeuPheGluThrLys 246
    |||||
Db 900 CTGCTTTTGAACCTAAG 917

RESULT 2
US-09-188-930-203
: Sequence 203, Application US/09188930A
: Patent No. 6150502
: GENERAL INFORMATION:
: APPLICANT: Watson, James D.
: APPLICANT: Strachan, Lorna
: APPLICANT: Sleeman, Matthew
: APPLICANT: Onrust, Rene
: APPLICANT: Murlison, James Greg
: TITLE OF INVENTION: Compositions Isolated From Skin Cells
: FILE REFERENCE: 11000.1011c1
: CURRENT APPLICATION NUMBER: US/09/188,930A
: NUMBER OF SEQ ID NOS: 348
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 203
: LENGTH: 1123
: TYPE: DNA
: ORGANISM: Rat
US-09-188-930-203
Alignment Scores:

```

```

Pred. No.: 1,21e-117 Length: 1123
Score: 1311.00 Matches: 236
Percent Similarity: 97.15% Conservative: 3
Best Local Similarity: 95.93% Mismatches: 7
Query Match: 95.90% Indels: 0
DB: 3 Gaps: 0

US-10-036-041-2 (1-246) x US-09-188-930-203 (1-1123)
QY 1 MetLeuThrArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPheLeuProPheCys 20
    |||||
Db 180 ATGCTCAGAGAGCGAGCTCGTGTGTGGACACTGCTGTGCTTTCTTCCTCCATTTTGC 229
QY 21 LeuCySGlnAspGluTyrMetGluSerProGlnThrGlyLeuProAspCysSer 40
    |||||
Db 240 CTGTCTCAAGATGAAATACATGAGTCTCCACAAGCTGAGAGACTGCCCCAGACTGCAGC 299
QY 41 LysCysCySHisGlySprSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
    |||||
Db 300 AAGTGTTCATGAGATGATGATTCCTGCTGTTACCAAGGCGCCCTTGAGCCCAAGGT 359
QY 61 ProProGlyIleProGlyLysnHisGlyAsnAsnGlyLysnAsnGlyAlaThrGlyHisGlu 80
    |||||
Db 360 CCGCTCGGATTCAGAGAAACCTGGAACAATGGAATACGAGAGCCACTGGCCAGAA 419
QY 81 GlyAlaLysGlyGlyLysGlyAspLysGlyAspLeuGlyProArgGlyLysGlyGln 100
    |||||
Db 420 GGGGCCCAAGGTCAGAAAGAGACAAAGGCGACCTGGGCGCTGAGGGGGAAGCGGGCAG 479
QY 101 HisGlyProLysGlyLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120
    |||||
Db 480 CATTGGCCCAAGGATGAGAGATACCCAGGGGGTGCACAGAGCTGCAGATTGGCTTC 539
QY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
    |||||
Db 540 ATGGCTTCTCTACCGACTCACTTACAGCAATCAGAACAGTGGCATTTATCTTCAGCAGTGT 599
QY 141 GluThrAsnIleGlyAsnPheAspValMetThrGlyArgPheGlyAlaProValSer 160
    |||||
Db 600 GAGACCAACATTGGAACACTCTTCGATGTCATGATGATGATTTGGGCGCCCGTATCA 659
QY 161 GlyValTyrPhePheThrPheSerMetMetLysHisGlyAspValGluGluValTyrVal 180
    |||||
Db 660 GCGGTGTATTTCTTCACCTTCACCATGATGAAATGAGACCTGAGAGAGTATGTTG 719
QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetLysSerTyrGlnMetLysGlyLys 200
    |||||
Db 720 TACCTTATGACACATGTAACACGAGTGTTCAGCATGTACAGCTATGAAACAAAGGAGAAA 779
QY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPleu 220
    |||||
Db 780 TCAGATACATCCAGCAACCATGAGTGCATGAACTGGCCAAAGAGATGATGAGTGTG 839
QY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
    |||||
Db 840 AGAATGGCAAGCGTCCCTCCATGGGAGCCACAGCGCTTCTCTACCTTCGACGCTTT 899
QY 241 LeuLeuPheGluThrLys 246
    |||||
Db 900 CTGCTTTTGAACCTAAG 917

RESULT 3
US-09-188-930-217
: Sequence 217, Application US/09188930A
: Patent No. 6150502
: GENERAL INFORMATION:
: APPLICANT: Watson, James D.
: APPLICANT: Strachan, Lorna
: APPLICANT: Sleeman, Matthew
: APPLICANT: Onrust, Rene
: APPLICANT: Murlison, James Greg
: TITLE OF INVENTION: Compositions Isolated From Skin Cells

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FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 217
LENGTH: 1107
TYPE: DNA
ORGANISM: Rat
US-09-188-930-217

Alignment Scores:
Pred. No.: 1,136-21 Length: 1107
Score: 316.00 Matches: 86
Percent Similarity: 42.628 Conservative: 41
Best Local Similarity: 28.868 Mismatches: 89
Query Match: 23.12% Indels: 82
DB: 3 Gaps: 12

US-10-036-041-2 (1-246) x US-09-188-930-217 (1-1107)
OY 6 Leu11eTyrTrpGlnLeuAlaLeuPheLeuProPheCysLeuGlnAspGlu 25
DB 174 ATGATCTCTCGATGCTCTTGACCTGT-----GGCTCTCCG-----TGTCCTCGTAC 221
OY 26 TyrMet-----GluSerProGlnThrGlyGlyLeuProProAspCys 39
DB 222 CCATGCTTGGTGCCTTTCCTCGACGACTTCACAGAGGGTGTCTCACTGCTGTC 281
OY 40 SerLysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProGlyPro 59
DB 282 AGT-----CTGCCTGCTCCCAAGGCCACCT 308
OY 60 GlyProGly11LeuProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHis 79
DB 309 GGGCCCTCCAGAGACACAGGATCTCAGAAATGGATGGTTTCTGCTGAAG 368
OY 80 GluGlyAlaLysGlyLysGlyAspLysGlyAsp----- 91
DB 369 GATGGCCAGACGGCCAGACGAGACGAGGGGACAGTGGACAGAGAGTCCACTGCC 428
OY 92 -----Leu 92
DB 429 AGGACAGGACCGAGGAAACAAGACCAAGGCAAGCTGGGCCATGGGAGAGG 488
OY 93 GlyProArgGlyLysArg-----GlyGln 100
DB 489 GGTCTCTGAGAGCCCAAGGGGTCAAGTGTATCCCGGAACATGTATACCGGCAAG 548
OY 101 HisGlyProLysGlyLysGlyTyrProGly11LeuPro----- 113
DB 549 AAGGAGCTTAAGAGGAAAGGGAACCTGGCTCCAGGCCCTGTAGCTGGCGAGT 608
OY 114 ProGluLeuGln11LeuAlaPheMetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSer 133
DB 609 AGCCGACCCAGAGTGGCTTTTGGTGGCGGTAAACCAAGGTTACCACTAGCGGCACTG 668
OY 134 Gly11LeuPheSerSerValGluThrAsn11GlyAsnPhePheAspValMetThrGly 153
DB 669 CCCATCAAGTTTGCACAAGATTCGATGATGAGGAGGACACATGATGATCCAGTGGC 728
OY 154 ArgPheGlyAlaProValSerGlyValTyrPhePheThrPheSerMetMet----- 170
DB 729 AACTTGTCTGACGCTGCGAGGAGCTTATCTTACCTTACATACATACCTAGCGGCCAAC 788
OY 171 LysHisGlnAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsnThrValPhe 190
DB 789 AAACAC-----CTGCCATGCGGCTTAATGACAAATGGCCAG-----TAC 827
OY 191 SerMetLysSerTyrGluMetLys--GlyLysSerAspThrSerSerAsnHisAlaVal 209
DB 828 CGCATTCGACATTTTACGCCAACAACCGGCAACACAGACGCTGGCTGGGCTCCACCATC 887

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OY 210 LeuLysLeuAlaLysGlyAspGluValTyrPheArgMet-----GlyAsnGly 225
DB 888 CTAGCTCTCAAGAGGAGGATGATGATGCTGCTTACAGATTTTCTACTCGAGACGATGGA 947
OY 226 AlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPhe 243
DB 948 CTCTTCTACGACCTTATTTGACCGACGACGCTTTCACCGGCTTCTCATCTAC 1001

RESULT 4
US-08-463-911-1
Sequence 1, Application US/08463911
Patent No. 5869330
GENERAL INFORMATION:
APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SPERM PROTEIN PRODUCED
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,911
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI95-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1276 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 46..786
US-08-463-911-1

Alignment Scores:
Pred. No.: 5,98e-20 Length: 1276
Score: 299.00 Matches: 82
Percent Similarity: 47.10% Conservative: 40
Best Local Similarity: 31.668 Mismatches: 103
Query Match: 21.87% Indels: 34
DB: 2 Gaps: 9

US-10-036-041-2 (1-246) x US-08-463-911-1 (1-1276)
OY 4 ArgGlnLeu11eTyrTrpGlnLeuAlaLeuPheLeuProPheCysLeuGln 23
DB 43 AGGATCTCTGCTGTCAGAGCTCTGCTTCTCTTAATCCTGCC--AGTCATGCCGA 99
OY 24 AspGluTyrMetGluSerProGlnThrGly-----LeuProProAspCysSerLys 41
DB 100 GATGAGCTTACTACATCACTAGAGAGTACTGCTGCTTGTGCTCTCCACCAAGGAGACT 159
OY 42 CysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProGlyProGlyPro 61
DB 111

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Db 160 TGTGCA-----GCTTCGATGCGA-----GGCATC 183
QY 62 ProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGly 81
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 184 CCAAGACATCTCTGCCACATGACACACAGCGGTGATGACAGATGACATCTCTGGA 243
QY 82 AlAlaGlyIleGlyGlyAspGlyAspLeuGlyProArgGlyGlyGly 98
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 244 GAGAAAGGAGAAAGAGATGACAGCTTCTTGCTTAAGGTGACAGAGATGTT 303
QY 99 GylGlnHisGlyProGlyIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 115
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 304 GGAATGACAGAGCTGAGAGCCAGGGGCTTCCCGGACCCCTGGCAGAGAAAGAGAG 363
QY 116 -----LeuGlnIleAlaPheMetAlaSerLeuAlaThrHisPhe 128
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 364 CCTGAGAACCGCTATATGATATGCTGACGCTTACGCTGGGGCTGGAGACCCGCTG 423
QY 129 SerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhe 148
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 424 ACTGTTCCCATGTACCCATTCCTTACTAAGATCTTCTACAAACCAAGAAATCATTTAT 483
QY 149 AspValMetThrGlyArgPheGlyAlaProValSerGlyValArgPheThrPheSer 168
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 484 GAGCGACAGCACTGCAAGTTCTACTGCAACATTCGGGACTTACTTACTTCTTACCA 343
QY 169 MetMetIleHisGlyAspValGluGluValValArgLeuMetHisAsnGlyAspThr 188
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 544 ATCAGCGTATC-----ATGAAAGATGTAGAGTGAAGCTTCTTCAAGAGAGCAAGGCC 597
QY 189 ValPheSerMetIleSerIleGlyMetIleGlyGlySerAspPheSerAsnHisAla 208
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 598 GTTCTCTTCCACACAGCAGATGACAGAAAGAAATGTGACAGGCCCTGTGCTGTG 657
QY 209 ValLeuIleSerLeuAlaGlyAspGluValThrPheArgMet---GlyAsnGly 225
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 658 CTCTCATCTGACAGGAGGAGACAGCAAGTGTGCTCAGGTATGGGATGGGAGCAC 717
QY 226 ---AlaLeuHisGlyAspHisGlyIleArgPheSerThrPheAlaGlyPheLeuPhe 243
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 718 AATGACTCTATGACAGATACGTCAACAGACTTACTGCTTCTTCTCTAC 774

```

RESULT 5  
US-08-463-911-6  
Sequence 6, Application US/08463911  
Patent No. 5869330  
GENERAL INFORMATION:

APPLICANT: Scherer, Philipp E.  
APPLICANT: Lodish, Harvey F.

TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED  
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:  
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Millenia Drive  
CITY: Lexington

STATE: Massachusetts  
COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,911.  
FILING DATE:

CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: WHI95-05  
TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: COS
LOCATION: 73..804
US-08-463-911-6

Alignment Scores:
Pred. No.: 2,11e-19 Length: 1313
Score: 293.50 Matches: 82
Percent Similarity: 46.47% Conservative: 43
Best Local Similarity: 30.48% Mismatches: 97
Query Match: 21.47% Indels: 48
DB: Gaps: 11

US-10-036-041-2 (1-246) x US-08-463-911-6 (1-1313)
QY 9 TrpGlnLeuLeuAlaLeuPheLeuProPhe-----CysLeuGly 23
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 26 TATCAATTCCTCGCTGCGGTCTGATTCATACAGAGGGCTCAGAGATCTGTCTGG 85
QY 24 AspGluArg-----MetGluSerProGlnIleGly 34
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 86 GAGCTGTCTACTCTCTATTAGCTGTCCCGGTACACCAAGAAACCAAGCACTCAAGGC 145
QY 35 LeuProProAspCysSerIleGlyGlyAspPheArgGlyArgGly 175
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 146 ---CCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 175
QY 55 ProProGlyProProGlyProProGlyIleProGlyAsnHisGlyAsnGlyAsn 74
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 176 ---CCTCACAGCGTGGATG-CCGCGCATCCAGCGCATCCGCGCATTAATGCGCCCA 231
QY 75 GlyAlaThrGlyHisGlyIleGlyAlaGlyIleGlyAspGlyAspGlyAsp 91
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 232 GCGCGTATGCGCAGAGATGCGCAGCCCTGGTGAGAGGCTGAGAAAGAGATCCAGTCTT 291
QY 92 LeuGlyProArg-----GlyGluArgGlyGlnHisGlyProGlyGlyGly 108
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 292 ATTCGCTCTAAGGAGACATCGTGAACCGGAGTACCCGGGCTGAAGTCCCGCAGGC 351
QY 109 TyrProGlyIle-----ProProGlu-----LeuGlnIle 118
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 352 TTTCGCGGAATCCAAAGCAGAGAAAGAGAACTGGAAGAGTGCCTATGATACCGCTCA 411
QY 119 AlaPheMetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSer 138
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 412 GCATTCAGTGTGAGATGAGACTTACGTATCCCAACATGCCATTCGCTTATAC 471
QY 139 SerValGluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaPro 158
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 472 AAGATCTTACAAATCAACCAAAACCACTATGATGCTCCACTGTAATTCACCTGAAC 531
QY 159 ValSerGlyValTyrPhePheThrPheSerMetMetIleHisGlyAspValGluGluVal 178
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 532 ATTCCTGGGCTGTACTCTTCCCTACACATCACTAT-----ATGAGAGATGTG 585
QY 179 TyrValTyrLeuMetHisAsnGlyAsnThrValPheSerMetIleSerIleGlyMetIle 198
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 586 AAGTCAGCTCTTCAAGAGAGACAGCAAGCTATGCTTCACTATGATCACTACAGAA 645
QY 199 GlySerAspThrSerSerAsnHisAlaValLeuIleGlyAspGlyVal 218
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 646 AATAATGTGACAGCGCTCCGCTCTGCTCTGATGTGACAGTGGGAGCAAGT 705
QY 219 TrpLeuArgMet---GlyAsnGly-----AlaLeuHisGlyAspHisGlnArgPhe 234

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|  |     |   |     |
|--|-----|---|-----|
| Db   | 706 | TGGCTCCAGGCTGTAATGGGAAAGAGACCGCTAATGCACTATATGCTGATATATGACAATGAC | 765 |
| QY   | 235 | SerThrProLeuAlaGlyPheLeuLeuPhe                                  | 243 |
| Db   | 766 | TCCACCTTCACAGCGCTTTCCTCTCTAC                                    | 792 |
| RESULT 6   |     |   |     |
| US-09-140-804-9  |     |   |     |
| Sequence 9, Application US/09140804                    |     |   |     |
| Patent No. 6197930                                     |     |   |     |
| GENERAL INFORMATION:                                   |     |   |     |
| APPLICANT: Sheppard, Paul O.                           |     |   |     |
| TITLE OF INVENTION: ADIPOCTE-SPECIFIC PROTEIN HOMOLOGS |     |   |     |
| FILE REFERENCE: 97-49                                  |     |   |     |
| CURRENT APPLICATION NUMBER: US/09/140,804              |     |   |     |
| CURRENT FILING DATE: 1998-08-26                        |     |   |     |
| EARLIER APPLICATION NUMBER: 60/056,983                 |     |   |     |
| EARLIER FILING DATE: 1997-08-26                        |     |   |     |
| NUMBER OF SEQ ID NOS: 47                               |     |   |     |
| SOFTWARE: FastSeq for Windows Version 3.0              |     |   |     |
| SEQ ID NO 9  |     |   |     |
| LENGTH: 4517   |     |   |     |
| TYPE: DNA  |     |   |     |
| ORGANISM: Homo sapiens                                 |     |   |     |
| US-09-140-804-9  |     |   |     |
| Alignment Scores:                                      |     |   |     |
| Pred. No.: 1,14e-18 Length: 4517                       |     |   |     |
| Score: 293.50 Matches: 83                              |     |   |     |
| Percent Similarity: 47.45% Conservative: 38            |     |   |     |
| Best Local Similarity: 32.55% Mismatches: 96           |     |   |     |
| Query Match: 21.47% Indels: 39                         |     |   |     |
| DB: 4 Gaps: 11   |     |   |     |
| US-10-036-041-2 (1-246) x US-09-140-804-9 (1-4517)     |     |   |     |
| QY   | 9   | TrpGlnLeuAlaLeuPheLeuProPheCysLeuGlyGlnAspGluTyrMetGlu          | 28  |
| Db   | 37  | TGGAGCTG-----TTCTACTGGCTATAGCTGTGCGCGGCG--ATGACACAGG            | 81  |
| QY   | 29  | SerProGlnThrGlyGlyLeuProProAspCysSerIscysCysHisGlyAspTyrSer     | 48  |
| Db   | 82  | AAACACAGCACTCAAGGCG--CCGAGATCCTCGTCCCTCCGCCAAGGGG-----          | 129 |
| QY   | 49  | PheArgGlyTyrGlnGlyProProGlyProProGlyProProGlyIleProGlyAsnHis    | 68  |
| Db   | 130 | -----CTGCACAGAGTTGGATG-GGGGGCACTCCAGGGCATCCG                    | 167 |
| QY   | 69  | GlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlnGlyAlaIleGlyGlyGlyAsp       | 88  |
| Db   | 168 | GGCCATATATGGGCGCCGACGCCCGATGGACGAGATGGCAACCCGTGTGAAGAGGTGAG     | 227 |
| QY   | 89  | LysGlyAsp-----LeuGlyProArg-----GlyIleuArgGlyGlnHisGly           | 102 |
| Db   | 228 | AAAGAGATCCAGGCTCTTAATGTGCTCAAGGAGACATCGTGAACCGAGATACCCGGG       | 287 |
| QY   | 103 | ProLysGlyGlyLysGlyTyrProGlyIle-----ProProGlu---                 | 115 |
| Db   | 288 | GCTGAAAGGTCCCGAGGCTTTCGCGGAATCCACAGCGAAGAGACCTGGAGAGGT          | 347 |
| QY   | 116 | -----LeuGlnIleAlaPheMetAlaSerLeuAlaThrHisPheSerAsnGlnAsn        | 132 |
| Db   | 348 | GCCATGATGATACCGCTCAGCATGATAGTGGGATTTGGAGACATTACCTTATATCCCAAC    | 407 |
| QY   | 133 | SerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPheAspValMetThr       | 152 |
| Db   | 408 | ATGCCCATTCCTCTTACCAAGATCTTCAACAATGACAAAACCACTATGATGGCTCCACT     | 467 |
| QY   | 153 | GlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPheSerMetMetLysHis    | 172 |
| Db   | 468 | GGTAATTCACCTGCACAACTATCTGGCTGTAGTACTATTCCTTACACATACACAGCTAT     | 527 |

|  |      |   |          |
|--|------|---|----------|
| Oy   | 173  | GLUSPRLGLGUGLUALTYRVALTYRLEMEHISASNGLYASNHYALPHESERMET        | 192      |
| Db   | 528  | -----ATGAAGATGTCGAAGGTCACGCTTTCACAAAGACAGGCTATGCTTTCAC        | 581      |
| Oy   | 193  | TYRSERTYRGUJMETLYSGLYLSSEASPRHSEASRNHISALVALLEULYSLEU         | 212      |
| Db   | 582  | TATGATCAGTACACAGAAATAATGTGGACACAGCCCGCGCTGTGCTCTGCATCG        | 641      |
| Oy   | 213  | ALALYSGLYSPGLUALITTPLEUAHGMET---GLYASNGLY-----ALALEUHI        | 228      |
| Db   | 642  | GAGGTGGCGCCAGCAAGCTGTGCTTCAGGTGTAGGGGAAGAGGCTAATGAGCTTAT      | 701      |
| Oy   | 229  | GLYASPHISGLNAHYPHESERTHRPHEALGLYPHEULEUPHE                    | 243      |
| Db   | 702  | GCTGATATGACATGACATGACTCCACTTCACAGGCTTCTCTCTAC                 | 746      |
| RESULT 7   |      |   |          |
|  |      | US-09-370-838-151   |          |
|  |      | : Sequence 151, Application US/09370838                       |          |
|  |      | : Patent No. 6444425  |          |
|  |      | : GENERAL INFORMATION:  |          |
|  |      | : APPLICANT: Reed, Steven G.                                  |          |
|  |      | : APPLICANT: Lodes, Michael J.                                |          |
|  |      | : APPLICANT: Mohamath, Roadoh                                 |          |
|  |      | : APPLICANT: Secrist, Heather                                 |          |
|  |      | : TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF  |          |
|  |      | : TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE   |          |
|  |      | : FILE REFERENCE: 210121.475C1                                |          |
|  |      | : CURRENT APPLICATION NUMBER: US/09/370,838                   |          |
|  |      | : EARLIER FILING DATE: 1999-08-09                             |          |
|  |      | : EARLIER APPLICATION NUMBER: US 09/285,323                   |          |
|  |      | : EARLIER FILING DATE: 1999-04-02                             |          |
|  |      | : NUMBER OF SEQ. ID NOS: 289                                  |          |
|  |      | : SOFTWARE: FASTSEQ for Windows Version 3.0                   |          |
|  |      | : SEQ ID NO 151   |          |
|  |      | : LENGTH: 3275  |          |
|  |      | : TYPE: DNA   |          |
|  |      | : ORGANISM: Homo sapien                                       |          |
|  |      | US-09-370-838-151   |          |
| Alignment Scores:                                    |      |   |          |
|  |      | Pred. No.:  | 6.96e-17 |
|  |      | Score:  | 273.00   |
|  |      | Percent Similarity:   | 47.33%   |
|  |      | Best Local Similarity:  | 29.63%   |
|  |      | Query Match:  | 19.97%   |
|  |      | DB:   | 4        |
|  |      |   | Gaps: 8  |
| US-10-036-041-2 (1-246) x US-09-370-838-151 (1-3275) |      |   |          |
| Oy   | 34   | GLYLEUPROPOROLASPCYSSERYSCYSHISGLYASPRYSER                    | 48       |
| Db   | 2064 | GGACTTCCTT-----TCAATTCCAAATGAAATTAATAGCCAGCTGCAGTTCCAA        | 2111     |
| Oy   | 49   | PHEATRGGLTYRGNGLYRPROPO-----                                  | 56       |
| Db   | 2112 | GCTHAGAGGATTTTGTGGACGACCTTATTTCCCAAGGATTAATTTCCAGCAGGTATTAG   | 2171     |
| Oy   | 57   | -----GLYRPROGILYRPROGILYRPROGILYRPROGILYASNHISGLYASNHISGLYASN | 74       |
| Db   | 2172 | CGAGAGGAGGACATGCTGTGTGCCACGAGCAAAATTCGAGAGCAGGCGTGAATTCCTT    | 2231     |
| Oy   | 75   | GLYLAHLAHLRGLYHISGLYUGLYALALYLSGLYULYLSGLYASPRYSLYSPREUGLYR   | 94       |
| Db   | 2232 | CAGGTGAGCCAGCCAGAA---AAGACACAAACCTTTACAGTGTGATCTTGACAA        | 2288     |
| Oy   | 95   | ARGLYGLYLAHRYGLYGLIN-----HISGLYRPROLYSGLYLU---                | 106      |
| Db   | 2289 | GGAACATCCCGTACACAGACCCTGTGGATGTGCCAGTGCACAAATTCACACCACCACTA   | 2348     |
| Oy   | 107  | -----LYSGLYYRPROGILYRPROGILYRPROGILYRPROGILYRPROGILYRPROGILY  | 123      |

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Db 2349 CTGCCAGTACAGCTTACCT---CTGCCCTACAGATGCGAGTGGCTTCTCAGACGCC 2405
QY 124 LeuAlaThrHisPheSer-----AsnGlnAsnSerGlyIleIlePheSerValGlu 141
Db 2406 AGAACCTGTAATGCGCCCTGGAACCTTAGACCAACCATCTATGTGTTGATCTTCTTCG 2465
QY 142 ThrAsnIleGlyAsnIlePheAspValMetThrGlyArgPheGluAlaProValSerGly 161
Db 2466 AACAACTTAGAAGAAACTTTGATCTTCACCTTGATGATTAATGATGCCAGGAATGGC 2525
QY 162 ValTyrPhePheThrPheSerMetMetLeuHisGlnAspValGluValTyrValTyr 181
Db 2526 ACTTACGTTTCAATTTTTCACATGCTAAAGCTGACATGATGCGACATGATGTCAC 2585
QY 182 LeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetGlyGlySer 201
Db 2586 CTCATGAGAAATGAGAGAGCTGTGATCAGCTATGCGCAATGATGCTGCTCAGACCAT 2645
QY 202 AspThrSerSerSerHisAlaValLeuValLeuValLeuValLeuValLeuValLeu 221
Db 2646 GAAACTGCTAGCATATCATGAAATCTTCACCTCTCCAGGAGACAGATATGTTACGT 2705
QY 222 MetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeu 241
Db 2706 CTCACAGAGGAGCAATTTATGAGAGAGTGGAAATATTCTACGTTTTCAGGCTATCTT 2765
QY 242 LeuPheGlu 244
Db 2766 CTTTATCAA 2774

RESULT 8
US-09-227-357-51
; Sequence 51, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; EARLIER FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
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; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (485)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (486)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (493)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (496)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (587)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (633)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1330)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-227-357-51

Alignment Scores:
Pred. No.: 1,35e-16 Length: 1333
Score: 264.50 Matches: 85
Percent Similarity: 40.288 Conservative: 31
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|                        |        |             |    |
|------------------------|--------|-------------|----|
| Best Local Similarity: | 29.51% | Mismatches: | 98 |
| Query Match:           | 19.35% | Indels:     | 75 |
| DB:                    | 4      | Gaps:       | 10 |

US-10-036-041-2 (1-246) x US-09-227-357-51 (1-1333)

[illegible]

RESULT 9

Sequence 1, Application US/09140804  
Patent No. 6197930  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Humes, Jacqueline M.

```

: TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
:
: FILE REFERENCE: 97-49
:
: CURRENT APPLICATION NUMBER: US/09/140, 804
:
: CURRENT FILING DATE: 1998-08-26
:
: EARLIER APPLICATION NUMBER: 60/056, 983
:
: EARLIER FILING DATE: 1997-08-26
:
: NUMBER OF SEQ ID NOS: 47
:
: SOFTWARE: FastSeq for Windows Version 3.0
:
: SEQ ID NO 1
:
: LENGTH: 1347
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: NAME/KEY: CDS
:
: LOCATION: (198)...(926)
:
: US-09-140-804-1

```

|                        |          |
|------------------------|----------|
| Alignment Scores:      |          |
| Pred. No.:             | 1,37e-16 |
| Score:                 | 264.50   |
| Percent Similarity:    | 48.028   |
| Best Local Similarity: | 32.608   |
| Query Match:           | 19.358   |
| DB:                    | 4        |
|                        | Gaps: 9  |

US-10-036-041-2 (1-246) x US-09-140-804-1 (1-1347)

|    |     |  |                                    |                         |    |
|----|-----|--|------------------------------------|-------------------------|----|
| Oy | 34  | GLYLeuPRoP----   | AspCysSerIu-----                   | CysCysHisGlyAspIuSerPhe | 49 |
|    |     |  |                                    |                         |    |
| Db | 240 | GGCTGGCCCCCACTGACGACACAAATAATCCCAAGCCTCTGGCCGGGG-----          | CAC                                | 2309                    |    |
| Oy | 50  | ArgGlyTyrGInGlyPRoPRoGlyPRoPRoGlyPRoPRoGlyIlePRoGlyAsnHisGly   | 69                                 |                         |    |
|    |     | ..   |                                    |                         |    |
| Db | 291 | CCCGGCTTCAGGACACCGCCGGGCGACACATGGCAAGCCAGGGCTTGGCCGGGCGGAAATGC | 350                                |                         |    |
| Oy | 70  | AsnAsnGlyAsnAsnGlyAlaThrGlyHisGluGlyAlaLysGlyIu-----           | 85                                 |                         |    |
|    |     | ..:  |                                    |                         |    |
| Db | 351 | CGCGACGCGCCGACGCGCGCCCGGGGCTCCGGGAAGAAAGCGGAGGCGGAGGCGG        | 410                                |                         |    |
| Oy | 86  | -----LysGlyAspLysGlyAspLysGlyPRoPRoGlyAlaThrGlyIleHisGlyPRo    | 1039                               |                         |    |
|    |     |  |                                    |                         |    |
| Db | 411 | GGATCGCCGGGACCTCGAGGGACCCGGGGCGGAGAGAGCGGAGCCCGGGGGCC          | 4707                               |                         |    |
| Oy | 104 | LysGlyGlyLysGlyTyrPRoGlyIlePRoPRoGlyIuGlnIleAlaPheMetAlaSer    | 1233                               |                         |    |
|    |     |  |                                    |                         |    |
| Db | 471 | ACCGGCGCTCCCGGGAGCTCGTGCTGCTCCGGGATCCGGCTTCACGGGCAAGCGCTCC     | 530                                |                         |    |
| Oy | 124 | LeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerValGlyThrAsn      | 1433                               |                         |    |
|    |     | :::  |                                    |                         |    |
| Db | 531 | GAGAGCCGGGTCCTCCGCGCTCGAGGACACCTTGGCTCTCGACCGCGTGGTGTAAC       | 590                                |                         |    |
| Oy | 144 | IleGlyAsnPhePheAspValMetThrGlyAlaPheGlyAlaPRoValSerGlyValTyr   | 163                                |                         |    |
|    |     | ..:  |                                    |                         |    |
| Db | 591 | GAGCAGGACATTTACGAGCGCGTACCGGAGATTTACCTGGCAGGGCTGGGGGTAC        | 650                                |                         |    |
| Oy | 164 | PhePheThrPheSerMetMetLysHisGlyAspValGlnGlyIuValTyr-----        | 181                                |                         |    |
|    |     | :::  |                                    |                         |    |
| Db | 651 | TACTTCCGCGTC-----  | CATGCCACGCTTCACGGGCGACGCTGACGTTGAT | 698                     |    |
| Oy | 182 | LeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGly-----    | 199                                |                         |    |
|    |     |  |                                    |                         |    |
| Db | 699 | CTGGTGAAGATGGCGAATCATTCATTCCTTTCTTCCAGATT--                    | TTCGGGGGCTGCC                      | 755                     |    |
| Oy | 200 | LysSerAspTrpSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGlyValThr   | 219                                |                         |    |
|    |     |  |                                    |                         |    |
| Db | 756 | AAGCCAGCCTGCTCTGGGGGGGGCATGGTGAAGCTGGAGCCTGAGACCAAGATGTGG      | 815                                |                         |    |
| Oy | 220 | LeuAlaGmetGlyAsnGly-----                                       | AlaLeuHisGlyAspHisGlnAlaPheSerThr  | 236                     |    |
|    |     | :::  |                                    |                         |    |
| Db | 816 | GTGCAAGGGGTGGGGGATACATTGGGATCTGAATGCGACATCAAGACAGACAGACC       | 875                                |                         |    |
| Oy | 237 | PheAlaGlyPheLeuLeuPhe  | 243                                |                         |    |
|    |     |  |                                    |                         |    |



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OY 164 PhePheThrPheSerMetMetLysHisGluAspValGluIleValTyr----- 181
   |||
   :|:|:|
Db 588 TACTTTGCTG-----CACGCCACTGCTACCGGGCCAGCTTCAGTTGAT 635
OY 182 LeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGly----- 199
   |||:|:|
   :|:|:|
Db 636 CTGTCAAAACAGGGGACATCCATCCCTTCTTCCAGTAT--TTGGGGGGGGGGCC 692
OY 200 LysSerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyr 219
   |||
   :|:|:|
Db 693 AAGCCAGCTTCGCTCTCAGGGGGTCCGATGGAAGCTAGAACCTGAGGACCGAGTGG 752
OY 220 LeuArgMetGlyAsnGly-----AlaLeuHisGlyAspHisGlnArgPheSerThr 236
   |||:|:|
   :|:|:|
Db 753 GTGCGAGTGGGGCTGGGATTAATGATGTCATATGCCAGCATCAGACAGACAGTACC 812
OY 237 PheAlaGlyPheLeuLeuPhe 243
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   :|:|:|
Db 813 TTCTCTGATTTCTCTCTAT 833

RESULT 12
US-09-188-930-30
: Sequence 30, Application US/09188930A
: Patent No. 6150502
: GENERAL INFORMATION:
: APPLICANT: Watson, James D.
: APPLICANT: Strachan, Lorna
: APPLICANT: Sleeman, Matthew
: APPLICANT: Onrust, Rene
: APPLICANT: Murison, James Greg
: TITLE OF INVENTION: Compositions Isolated From Skin Cells
: FILE REFERENCE: 11000.1011c1
: CURRENT APPLICATION NUMBER: US/09/188,930A
: CURRENT FILING DATE: 1998-11-09
: NUMBER OF SEQ ID NOS: 348
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 30
: LENGTH: 1015
: TYPE: DNA
: ORGANISM: Rat
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (545)...(545)
US-09-188-930-30

Alignment Scores:
Pred. No.: 8,59e-16 Length: 1015
Score: 254.50 Matches: 79
Percent Similarity: 45.78% Conservative: 35
Best Local Similarity: 31.73% Mismatches: 100
Query Match: 18,62% Indels: 35
DB: Gaps: 10

US-10-036-041-2 (1-246) x US-09-188-930-30 (1-1015)
OY 11 LeuLeuAlaLeuPhePheLeuProPheCysLeuCysGlnAspGluTyrMetGluSerPro 30
   |||
   :|:|:|
Db 221 CTCTTCTCCCTCTGCTGCTGCTGCA----- 250
OY 31 GlnThrGlyGlyLeuProProAspCysSerLys-----CysCysHisGlyAspTyr 47
   |||:|:|
   :|:|:|
Db 251 ---TCAGGCTCTCTCTCTGAGACACAAATCCACACCTGTCCTGGCAG--- 304
OY 48 SerPheArgGlyTyrGlnGlyProProGlyProProGlyIleProGlyAsn 67
   |||
   :|:|:|
Db 305 -----CCCGGCTCCAGGACACACAGCCACCCAGCCAGGCTCCCTGGCCGT 358
OY 68 HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlnGluAlaLysGly 87
   |||
   :|:|:|
Db 359 GAGGAGCCCTGAGCCGAGGAGGAGACCCGAGCTCCGGGAGAGAAAGGAGGAGGCGG 418
OY 88 AspyrGlyAspLeuGlyProArgGlyGlu-----ArgGlyGlnHisGlyProLys 104

```

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Db 419 AGACGGGACCTACCTGGGCCACAGTGGGAGCCCGGGCCGCGAGAGACAGACCTGTG 478
OY 105 GlyGluLysGlyTyrProGly-----IleProProGluLeuGlnIleAlaPheMet 121
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   :|:|:|
Db 479 GGGGCTATCGGGCCCTCGCGGGGAGTCTCGGTGGCCGACAGTACAGCTTCAGTCCAG 538
OY 122 AlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerValGlu 141
   |||
   :|:|:|
Db 539 CGATATAGAGCCGGGTACCTCCGCCAGCCACACACCCCTACCTTCGACCGCTGGCG 598
OY 142 ThrAsnIleGlyAsnPheAspValMetThrGlyArgPheGlyAlaProValSerGly 161
   |||
   :|:|:|
Db 599 CTCATGACGACGAGCATATTACATGACCTACCGGCAAGTTCACCTGCCAAGCTCGCT 658
OY 162 ValTyrPhePheThrPheSerMetLysHisGluAspValGluIleValTyrValTyr 181
   |||:|:|
   :|:|:|
Db 659 GTCTACTACTTTCCTGTC-----CATGCCACTGTCTACCGGGCCAGCTACAG 706
OY 182 -----LeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGly 199
   |||:|:|
   :|:|:|
Db 707 TTGTATCTTGTCAAAATAGCCCATCATGACTTCTTCTTCAGTTT--TTGGGGGG 763
OY 200 -----LysSerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGlu 217
   |||
   :|:|:|
Db 764 TGGCCAAAGCCAGCTCGCTCAGGGGGTGGCATGTGATGAGCTAGAACCTGAGACAG 823
OY 218 ValTyrPheArgMetGlyAsnGly-----AlaLeuHisGlyAspHisGlnArgPhe 234
   |||:|:|
   :|:|:|
Db 824 GTATGGGTTTCAGGTGGGTGGGTGATTAATGATTCATTCGATTCAGCATCAGCATCAAGAC 883
OY 235 SerThrPheAlaGlyPheLeuLeuPhe 243
   |||:|:|
   :|:|:|
Db 884 AGTACCTTCTCTGATTTCTCTAT 910

RESULT 13
US-09-188-930-218
: Sequence 218, Application US/09188930A
: Patent No. 6150502
: GENERAL INFORMATION:
: APPLICANT: Watson, James D.
: APPLICANT: Strachan, Lorna
: APPLICANT: Sleeman, Matthew
: APPLICANT: Onrust, Rene
: APPLICANT: Murison, James Greg
: TITLE OF INVENTION: Compositions Isolated From Skin Cells
: FILE REFERENCE: 11000.1011c1
: CURRENT APPLICATION NUMBER: US/09/188,930A
: CURRENT FILING DATE: 1998-11-09
: NUMBER OF SEQ ID NOS: 348
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 218
: LENGTH: 1001
: TYPE: DNA
: ORGANISM: Rat
US-09-188-930-218

Alignment Scores:
Pred. No.: 1.31e-15 Length: 1001
Score: 252.50 Matches: 79
Percent Similarity: 45.78% Conservative: 35
Best Local Similarity: 31.73% Mismatches: 100
Query Match: 18,47% Indels: 35
DB: Gaps: 10

US-10-036-041-2 (1-246) x US-09-188-930-218 (1-1001)
OY 11 LeuLeuAlaLeuPhePheLeuProPheCysLeuCysGlnAspGluTyrMetGluSerPro 30
   |||
   :|:|:|
Db 207 CTCTTCTCCCTCTGCTGCTGCTGCA----- 236
OY 31 GlnThrGlyGlyLeuProProAspCysSerLys-----CysCysHisGlyAspTyr 47

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Db      237  ---TCAGGCTCTCTCTCTGAGACAGACAGATCCCGAGCTGTGTCTCCCGGGCAG--- 290
Qy      48  SerPheArgGlyTyrGlnGlyProProGlyProProGlyIleProGlyIleProGlyAsn 67
Db      291  -----CCGGCCCTCCAGGACACAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 344
Qy      68  HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlyGlnAlaAlaGlyGlyGly 87
Db      345  GAGCGCCGTGATGCGCCGAGCGGTCAGACCCGAGCGCTCCGGAGAGAAAGCGAGCGCGG 404
Qy      88  AspIleGlyAsnGlyLeuGlyProArgGlyGlu-----ArgGlyGlnHisGlyProGly 104
Db      405  AGACCGGAGCTACCTGCGGACAGCGGAGCCCGGCGCGGAGAGAGAGAGAGAGAGAGAGAG 464
Qy      105  GlyGlyLeuGlyTyrProGly-----IleProProGlyLeuGlnIleAlaPheMet 121
Db      465  GGGGCTATCGGGCTCGGGGGGAGCTGCTCGGTCGCCAGGATGAGCTTCACTGAGCCAG 524
Qy      122  AlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerValGlu 141
Db      525  CGATCAGAGAGCGCGGATCTCCGCCAGACACACCCCTTACCCCTTGAGCCGTGCTG 584
Qy      142  ThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSerGly 161
Db      585  CTCATGTAGCAGGAGACATTCAGATGCCACTGACCGGCAAGTTCACCTGCCAAGTCCCTGT 644
Qy      162  ValTyrPhePheThrPheSerMetMetLeuHisGlnAspValGlnGluValTyrValTyr 181
Db      645  GTCTACTACTTGTCTGCTC-----CATGCCACTGTCTTACCGGGCCAGCCCTTACAG 692
Qy      182  -----LeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGlnMetLeuGly 199
Db      693  TTTCATGATTTGCAAAATGGCCATCATGCTCTTCTTCTCCAGTTT---TTGGGGGG 749
Qy      200  -----LysSerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGlu 217
Db      750  TGGCCAAAGACCACTGCTCTCTCAGGCGGTGCGATGCTGAGGCTGAGAACCTGAGGACAG 809
Qy      218  ValTyrPheLeuArgMetGlyAsnGly-----AlaLeuHisGlyAsnHisGlnAlaArgPhe 234
Db      810  GATGAGGCTTCAAGTGGGTGGTGGGATGATTGATTCATGGCATTCATGCCAGCATCAAAACAGAC 869
Qy      235  SerThrPheAlaGlyPheLeuPhe 243
Db      870  AGTACCTTCTCTGATTTCTCTGCTAT 896

RESULT 14
US-09-336-536-2
; Sequence 2, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336, 536
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-336-536-2

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Alignment Scores:
Pred. No.: 1,19e-15      Length: 728
Score: 251.00           Matches: 74
Percent Similarity: 48.028      Conservative: 35
Best Local Similarity: 32.608    Mismatches: 93
Query Match: 18,368           Indels: 26

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DB:      4      Gaps:      9
US-10-036-041-2 (1-246) x US-09-336-536-2 (1-728)
Qy      34  GlyLeuProPro---AspCysSerLys-----CysGlyHisGlyAspTyrSerPhe 49
Db      43  GGCTGCCCCCTGAGCAGACACAAAGATCCAGCCCTGCCCCGGG-----CAC 93
Qy      50  ArgGlyTyrGlnGlyProProGlyProProGlyIleProGlyIleProGlyAsnHisGly 69
Db      94  CCGGCGCTTCAGGACAGCGCGGACCATGACAGCCAGGAGCTTCCGGGCGCCGATGAC 153
Qy      70  AsnAsnGlyAsnAsnGlyAlaThrGlyHisGlyGlnAlaAlaGlyGlyGly 86
Db      154  CGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGAGAAAGAGAGAGG-CCGAGAGCG 212
Qy      87  -----GlyAspLysGlyAsnGlyProArgGlyGluArgGlyGlnHisGlyPro 103
Db      213  GAGCTGCGCGGAGCTCGAGGAGACCCCGGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAG 272
Qy      104  LysGlyGlyLeuGlyTyrProGlyIleProProGlyLeuGlnIleAlaPheMetAlaSer 123
Db      273  ACCGGGCTCCCGGGAGAGCTCTGCTGCTCCGAGTCCGCTTCAAGCCAGCGCTCC 332
Qy      124  LeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerValGluThrAsn 143
Db      333  GAGAGCGGGGTGCTCGCGCGCTGAGCAGACCCCTTGAGCCCTTGAGCCGCGCTGAGAAC 392
Qy      144  IleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTyr 163
Db      393  GAGCAGGAGACATTCAGCAGCGCGTACCGGCAAGTTCACCTGCCAAGTGCCTGGGGTCTAC 452
Qy      164  PhePheThrPheSerMetMetLeuHisGlnAspValGlnGluValTyrValTyr----- 181
Db      453  TACTTGGCCGCTC-----CATGCCAGCTTACCGGGCCAGCCCTTGCATTTGAT 500
Qy      182  LeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGlnMetLeuGly----- 199
Db      501  CTGCTGAAAGATGAGCGAATCATGCTCTTCTTCTCCAGTTT---TTGGGGGGGTGGGCC 557
Qy      200  LysSerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyr 219
Db      558  AAGCCAGCCCTGCTCTGCGGGGGGCGCATGCTGAGGCTGAGGCGAGCAGCAAGTGTGG 617
Qy      220  LeuArgMetGlyAsnGly-----AlaLeuHisGlyAsnHisGlnAlaArgPheSerThr 236
Db      618  GTCCAGGTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 677
Qy      237  PheAlaGlyPheLeuPhe 243
Db      678  TTCTCCGATTTCTGCTGATC 698

RESULT 15
US-09-336-536-1
; Sequence 1, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336, 536
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1338
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-336-536-1

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Alignment Scores:

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Pred. No.: 2.72e-15 Length: 1338  
Score: 251.00 Matches: 74  
Percent Similarity: 48.02% Conservative: 35  
Best Local Similarity: 32.60% Mismatches: 93  
Query Match: 18.36% Indels: 26  
DB: 4 Gaps: 9

US-10-036-041-2 (1-246) x US-09-336-536-1 (1-1338)

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OY 34 GlyLeuProPro---AspCysSerLys-----CysCysHisGlyAspTyrSerPhe 49
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DB 230 GGCCTGCCCCCTGACGACAAAGATCCACAGCTCTGCCGGG-----CAC 280
OY 50 ArgGlyTyrGlnGlyProProGlyProProGlyProProGlyLeuProGlyAsnHisGly 69
    ||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 281 CCCGCCCTTCACGAGCCCGGGCCACATGGCCAGCCAGGCTTCCGGCCGCGCATGGC 340
OY 70 AsnAsnGlyAsnAsnGlyAlaThrGlyHisGlnGlyAlaLysGlyGluLys----- 86
    ::||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 341 CCGGACGCGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 399
OY 87 -----GlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGlnHisGlyPro 103
    ||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 400 GCACTGCCGCGGACCTCGAGGGGACCCCGGGCGCGAGAGAGGCGGACCCCGGGCGCC 459
OY 104 LysGlyGluLysGlyTyrProGlyLeuProProGlyLeuGlnLeuAlaPheMetAlaSer 123
    ||| ||| ||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 460 ACCGGGCTGCGGGGAGTCTCGGGGCTTCGCGCATCCGCTTCAGCGCCAGCGCTCC 519
OY 124 LeuAlaThrHisPheSerAsnGlnAsnSerGlyLeuLeuPheSerSerValGluThrAsn 143
    ::||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 520 GAGACCGCGGCTCCCTCCGCGCTGACGACCCCTTGACCGCGCTGCGTGTGAAC 579
OY 144 IleGlyAsnPhePheAspValIleThrGlyArgPheGlyAlaProValSerGlyValTyr 163
    ::||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 580 GAGCAGGACATTAACGCGCTCAACGCGCAAGTTCACCTGCCAGGCTCGGGGTCTAC 639
OY 164 PhePheThrPheSerMetLeuHisGluAspValGluValTyr----- 181
    ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 640 TACTTCGCGCTC-----CATGCCACCGCTTACCGGGGCCAGCCTGCAGTTTGAT 687
OY 182 LeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGly----- 199
    ||||| ||||| ::||| ||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 688 CTGGTGAAGAATGGCAATCATGCTCTTCTTCCAGTTT---TTGGGGGGGTGGCCC 744
OY 200 LysSerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyr 219
    ||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 745 AAGCCAGCTCGCTCGGGGGGCGCATGTGAGGCTGAGGCTGAGGACCAAGTGTGG 804
OY 220 LeuArgMetGlyAsnGly-----AlaLeuHisGlyAspHisGlnArgPheSerThr 236
    ::||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 805 GTGCAGGTGGGTGTGGTACATACATTTGATGATGATGATGATGATGATGATGATGATGAT 864
OY 237 PheAlaGlyPheLeuLeuPhe 243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 865 TTCTCCGGAATTCTGGGTAC 885
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Search completed: January 15, 2003, 21:21:52  
Job time : 77 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 15, 2003, 19:39:50 ; Search time 3091 Seconds  
(without alignments)  
2316.173 Million cell updates/sec

Title: US-10-036-041-2  
Sequence score: 1367  
Sequence: 1 MLEWOLLYWOLALFLFLPFC.....LHGDHQRFTYFAGLLFETK 246

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2054640 segs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109380

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-DOCALLIGN-200 -THR\_SCORE-pct -THR\_MAX-100 -THR\_MIN-0 -ALIGN-15 -MODE-LOCAL  
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-YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

Database : GenEmbl:\*  
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2: gb\_htg:\*  
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7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
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13: gb\_un:\*  
14: gb\_vi:\*  
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16: em\_fun:\*  
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19: em\_mu:\*  
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29: em\_vi:\*  
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31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rtd:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID       | Description        |
|------------|--------|-------------|--------|-------------|--------------------|
| 1          | 1367   | 100.0       | 1696   | 6 AX039945  | AX039945 Sequence  |
| 2          | 1367   | 100.0       | 1709   | 6 AX136339  | AX136339 Sequence  |
| 3          | 1367   | 100.0       | 1710   | 9 AF329837  | AF329837 Homo sapi |
| 4          | 1367   | 100.0       | 1730   | 9 AF326976  | AF326976 Homo sapi |
| 5          | 1311   | 95.9        | 1117   | 6 AX039955  | AX039955 Sequence  |
| 6          | 1311   | 95.9        | 1879   | 10 AF246265 | AF246265 Mus muscu |
| 7          | 1291.5 | 94.5        | 1927   | 6 AX191537  | AX191537 Sequence  |
| 8          | 1259   | 92.1        | 810    | 6 AX136588  | AX136588 Sequence  |
| 9          | 1171   | 85.7        | 738    | 6 AX039954  | AX039954 Sequence  |
| 10         | 792.5  | 58.0        | 672    | 6 AX191527  | AX191527 Sequence  |
| 11         | 673    | 49.2        | 1426   | 9 BC016021  | BC016021 Homo sapi |
| 12         | 513.5  | 37.6        | 546    | 6 AX079496  | AX079496 Sequence  |
| 13         | 315    | 23.0        | 912    | 6 AX054802  | AX054802 Sequence  |
| 14         | 315    | 23.0        | 1306   | 9 AF329839  | AF329839 Homo sapi |
| 15         | 315    | 23.0        | 3959   | 9 BC022187  | BC022187 Homo sapi |
| 16         | 315    | 23.0        | 3959   | 9 BC024015  | BC024015 Homo sapi |
| 17         | 313    | 22.9        | 1236   | 10 BC030324 | BC030324 Mus muscu |
| 18         | 309    | 22.6        | 1282   | 6 AX054815  | AX054815 Sequence  |
| 19         | 306    | 22.4        | 1161   | 6 AX039965  | AX039965 Sequence  |
| 20         | 306    | 22.4        | 1176   | 9 AF329836  | AF329836 Homo sapi |
| 21         | 306    | 22.4        | 2404   | 9 BC011699  | BC011699 Homo sapi |
| 22         | 303    | 22.2        | 1134   | 4 AF269230  | AF269230 Bos tauru |
| 23         | 303    | 22.2        | 114675 | 2 AC010421  | AC010421 Homo sapi |
| 24         | 303    | 22.2        | 130630 | 2 AC010637  | AC010637 Homo sapi |
| 25         | 303    | 22.2        | 155013 | 2 AC026707  | AC026707 Homo sapi |
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| 28         | 299    | 21.9        | 1276   | 6 AR034252  | AR034252 Sequence  |
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| 32         | 297.5  | 21.8        | 777    | 10 AF095155 | AF095155 Mus muscu |
| 33         | 297.5  | 21.8        | 1297   | 9 AF095154  | AF095154 Homo sapi |
| 34         | 287.5  | 21.8        | 1526   | 9 BC008798  | BC008798 Homo sapi |
| 35         | 285.5  | 21.6        | 970    | 10 BC024634 | BC024634 Mus muscu |
| 36         | 295.5  | 21.5        | 2526   | 10 AB044560 | AB044560 Mus muscu |
| 37         | 293.5  | 21.5        | 734    | 9 AF040407  | AF040407 Macaca mu |
| 38         | 293.5  | 21.5        | 1313   | 6 AR034253  | AR034253 Sequence  |
| 39         | 293.5  | 21.5        | 4517   | 6 AR138194  | AR138194 Sequence  |
| 40         | 293.5  | 21.5        | 4517   | 6 AX195211  | AX195211 Sequence  |
| 41         | 293.5  | 21.5        | 4517   | 6 AX358529  | AX358529 Sequence  |
| 42         | 293.5  | 21.5        | 4517   | 6 AX358521  | AX358521 Sequence  |
| 43         | 293.5  | 21.5        | 4517   | 6 HUMUPST2  | D45371 Human apM1  |
| 44         | 293.5  | 21.5        | 4545   | 6 AX134174  | AX134174 Sequence  |
| 45         | 293    | 21.4        | 1152   | 6 AX195207  | AX195207 Sequence  |

RESULT 1

ALIGNMENTS

| AX039945 | LOCUS                                       | AX039945  | 1696 bp       | DNA  | linear | PAT 18-NOV-2000 |
|----------|---|---|---------------|------|--------|-----------------|
|          | DEFINITION                                  | Sequence 1 from Patent WO0063377.   |               |      |        |                 |
|          | ACCESSION                                   | AX039945  |               |      |        |                 |
|          | VERSION                                     | AX039945.1  | GI:11229969   |      |        |                 |
|          | KEYWORDS                                    |   |               |      |        |                 |
|          | SOURCE                                      | human.  |               |      |        |                 |
|          | ORGANISM                                    | Homo sapiens  |               |      |        |                 |
|          | REFERENCE                                   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. |               |      |        |                 |
|          | AUTHORS                                     | Piddington, C.S. and Bishop, P. D.  |               |      |        |                 |
|          | TITLE                                       | Adipocyte complement related protein homolog zacp3  |               |      |        |                 |
|          | JOURNAL                                     | Patent: WO 0063377-A 1 26-Oct-2000;   |               |      |        |                 |
|          |   | ZymoGenetics, Inc. (US)   |               |      |        |                 |
|          | FEATURES                                    | Location/Qualifiers   |               |      |        |                 |
|          | source                                      | 1..1696   |               |      |        |                 |
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|          |   | /db_xref="taxon:9606"   |               |      |        |                 |
|          |   | 69..809   |               |      |        |                 |
|          | CDS   | /note="unnamed protein product"   |               |      |        |                 |
|          |   | /codon_start=1  |               |      |        |                 |
|          |   | /protein_id="CAC16632.1"  |               |      |        |                 |
|          |   | /db_xref="GI:11229970"  |               |      |        |                 |
|          |   | /translation="MLMRQLIYQWLALFLEPRLCODEYMESRQTGLPPDSCKCH  |               |      |        |                 |
|          |   | GDSFSGTQGPFGPPGPIGNHNGNNGATGHEGAKGCKGGLGGRGGRGQHG   |               |      |        |                 |
|          |   | PKGEKGPGLPELQIALFMASLATHEENNSNGATIFSSVENIENGFEDVMGRGAPVS  |               |      |        |                 |
|          |   | GVYEFTEFSMKRHEDEVLEVYVYLHMGNGATVSMYSYEMKGSDDTSNNAVLAKGDEV   |               |      |        |                 |
|          |   | MLRGNALHGDHDFSTFAGFLFLEFK"  |               |      |        |                 |
|          | BASE COUNT                                  | 482 a 355 c 386 g 473 t   |               |      |        |                 |
|          | ORIGIN                                      |   |               |      |        |                 |
|          | Alignment Scores:                           |   |               |      |        |                 |
|          | Pred. NO.:                                  | 2,42e-96  | Length:       | 1696 |        |                 |
|          | Score:                                      | 1367.00   | Matches:      | 246  |        |                 |
|          | Percent Similarity:                         | 100.00%   | Conservative: | 0    |        |                 |
|          | Best Local Similarity:                      | 100.00%   | Mismatches:   | 0    |        |                 |
|          | Query Match:                                | 100.00%   | Indels:       | 0    |        |                 |
|          | DB:   | 6   | Gaps:         | 0    |        |                 |
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| QY       | 1   | MettLeuTPtAgtgInLeuIleTtTgplLeuLeuAlaLeuPheLeuProPheCys   | 20            |      |        |                 |
| DB       | 69  | ATGCTTTGGAGCGAGCTCATCTATTGGCAATGCTGCTGTTTCTCCCTTTTTC  | 128           |      |        |                 |
| QY       | 21  | LeucSGlnAspGluuTYrMetGluSerProGlnhrgGlyGlyLeuProAspCysSer   | 40            |      |        |                 |
| DB       | 129   | CTGTGTCAAGATGAATACATGAGAGTCTCCACAAACCGGAGGACTRACCCCGACTGCAGT  | 188           |      |        |                 |
| QY       | 41  | LysCysCysHisGlyAspTYrSerPheArgGlyTYrGlnGlyProProGlyProProGly  | 60            |      |        |                 |
| DB       | 189   | AAGGTGTTCATGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCTGGGGCCACGGGC   | 248           |      |        |                 |
| QY       | 61  | ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu  | 80            |      |        |                 |
| DB       | 249   | CTCTCTGCATTTCCACGAAACCATGAAACAAATGCAACATGAGACCATGTGCATGAA   | 308           |      |        |                 |
| QY       | 81  | GlyIleAluysGlyGlyIuysGlyAspIuysGlyAspIuysGlyProArgGlyGlyIuArgGlyGln   | 100           |      |        |                 |
| DB       | 309   | GGAGCCAAAGGTGAGAAAGGGCGAAGAAAGGTACTCTGGGGCTTCAGAGGGACCGGGGGCAG  | 368           |      |        |                 |
| QY       | 101   | HisGlyProLysGlyGlyIuysGlyTYrProGlyIleProProGlyIuLeuGlnIleAlaPhe   | 120           |      |        |                 |
| DB       | 369   | CATGGCCCCAAGAGAGAGAAAGGCTACCGGGGATTCACACAGAACTTCAGATTGCATTC   | 428           |      |        |                 |
| QY       | 121   | MetaLaserLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal  | 140           |      |        |                 |
| DB       | 429   | ATGGCTTCTGTGCACACCACTTCAGCAATCAGAAACAGTGAGATTACTTCAGCAGTGT  | 488           |      |        |                 |
| QY       | 141   | GluThrAsnIleGlyAsnPheAspValMetThrGlyArgPheGlyAlaProValSer   | 160           |      |        |                 |
| DB       | 489   | GAGACCAACATTTGGAACCTTTTGATGTACTATGACTGTAAATTTGGGCCCCAGATATCA  | 548           |      |        |                 |

|   |  |  |                 |
|---|--|--|-----------------|
| Qy  | 161  | GLYVALTYRPHENPETHRPHSESEMETMETYSHISGLUASPVALGLUGLVALTYRVAL     | 180             |
| Db  | 549  | GGGTGTATATTTCTTACCTTCAGCATGATGAAGACATGAGAGATGTCGAGCAAGCTGATATG | 608             |
| Qy  | 181  | TYRLEMETHISASGCIYASnthrValPheSerMetTyrSerTyrGluMetysGlyVs      | 200             |
| Db  | 609  | THCCTTATCACAAATGGCAGACACAGCTTTCACAGATGTACAGCTATGAATGAAGGCCAAA  | 668             |
| Qy  | 201  | SerAspThrSerSerAsnHisAlaValLeuTysLeuAlaLysGlyAspGluValTrpLeu   | 220             |
| Db  | 669  | TCAGATACATCCAGCAATCATCTGTCGTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTG    | 728             |
| Qy  | 221  | ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe   | 240             |
| Db  | 729  | CGAATGGCGAAATGGCGCTCTCCATGGGGACACCAACGCTTCCACACTTTCAGAGATTTC   | 788             |
| Qy  | 241  | LeuLeuPheGluThrLys   | 246             |
| Db  | 789  | CTGCTCTTTGAACCTAAG   | 806             |
| RESULT 2                                    |  |  |                 |
| AX136339                                    |  | 1709 bp  | DNA             |
| LOCUS                                       |  |  | Linear          |
| DEFINITION                                  | Sequence 261 from Patent EP1067182.  |  | PAT 30-MAY-2001 |
| ACCESSION                                   | AX136339   |  |                 |
| VERSION                                     | AX136339.1   | GI:14272745  |                 |
| KEYWORDS                                    |  |  |                 |
| SOURCE                                      | human.   |  |                 |
| ORGANISM                                    | Homo sapiens   |  |                 |
| REFERENCE                                   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.<br>1 (bases 1 to 1709)<br>Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and<br>Hayashi,K.<br>Secretory protein or membrane protein<br>Patent: EP 1067182-A 261 10-JUN-2001;<br>JOURNAL Helix Research Institute (JP) |  |                 |
| TITLE                                       |  |  |                 |
| AUTHORS                                     |  |  |                 |
| FEATURES                                    |  |  |                 |
| Source                                      | Location/Qualifiers  |  |                 |
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|   | /codon_start=1   |  |                 |
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|   | /db_xref="GI:14272746"   |  |                 |
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| BASE COUNT                                  | 480 a  | 363 c  | 390 g           |
| ORIGIN                                      |  |  | 476 t           |
| Alignment Scores:                           |  |  |                 |
| Pred. No.:                                  | 2,44e-96   | Length:  | 1709            |
| Score:                                      | 1367.00  | Matches:   | 26              |
| Percent Similarity:                         | 100.00%  | Conservative:  | 0               |
| Best Local Similarity:                      | 100.00%  | Mismatches:  | 0               |
| Query Match:                                | 100.00%  | Indels:  | 0               |
| DB:   | 6  | Gaps:  | 0               |
| US-10-036-041-2 (1-246) x AX136339 (1-1709) |  |  |                 |
| Qy  | 1  | MetLeuTPArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPheLeuProPheCys       | 20              |
| Db  | 89   | ATGCTTGGAGGACACTCATCTATTTGGCAAGCGTGGCTTTTCTCCTCCCTTTTGC        | 148             |
| Qy  | 21   | LeuYcGlnAspGluTyrMetGlnSerProGlnThrGlyGlyLeuProPheAspCysSer    | 40              |
| Db  | 149  | CTGTGTCAAGATGATATCATGTGAGTCTCCACAAACCGAGAGACTAACCCCGAGCTGCAGT  | 208             |

41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60  
DB 209 AAGTGTTCATGAGGAGCTACAGCTTTCGAGGCTACCAAGGCCCTCCGGCCACCGGGC 268  
61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80  
DB 269 CCTCGCATTCACGAGAACCATGGAACATGAGCAACATGAGCCACATGGTCATGAA 328  
81 GlyAlaIleGlyGluGlyGlyAspIleGlyAspIleGlyProArgGlyGluArgGlyGln 100  
DB 329 GGAGCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 388  
101 HisGlyProGlyGlyGluGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120  
DB 389 CATGGCCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 448  
121 MetAlaSerIleuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140  
DB 449 ATGGCTTCTCGGCAAGCCACTTCAGCATGAGACAGTGGGATATATCTTCAGCAGCTT 508  
141 GluThrAsnIleGlyAsnPheAspValMetThrGlyArgPheGlyAlaProValSer 160  
DB 509 GAGACCAACATGGAACTCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 568  
161 GlyValIleTyrPhePheThrPheSerMetIleGlyAspValGluGluValTyrVal 180  
DB 569 GGTGTGATTTCTTACCTTCAGCATGATGAGCATGAGCATGAGCATGAGCATGATGTG 628  
181 TyrIleuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200  
DB 629 TACCTTATGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 688  
201 SerAspThrSerSerAsnHisAlaValIleuLysIleuAlaIleGlyAspGluValTyrPhe 220  
DB 689 TCAGATACATCCAGAACATGCTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 748  
221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlyAsnArgPheSerThrPheAlaGlyPhe 240  
DB 749 CGAATGGCAATGGGCGCTCTCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 808  
241 LeuLeupheGluThrLys 246  
DB 809 CTGCTCTTGAACCTAAG 826

RESULT 3  
AF329837 1710 bp mRNA linear PRI 12-MAR-2001  
LOCUS Homo sapiens complement-clq tumor necrosis factor-related protein  
DEFINITION (CTRP3) mRNA, complete cds.  
ACCESSION AF329837  
VERSION AF329837.1 GI:13274519  
KEYWORDS Homo sapiens.  
SOURCE Homo sapiens.  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 1710)  
AUTHORS Piddington, C.S. and Bishop, P.  
JOURNAL Homo sapiens complement-clq tumor necrosis factor-related protein  
REFERENCE 2 (bases 1 to 1710)  
AUTHORS Piddington, C.S. and Bishop, P.  
TITLE Direct Submission  
JOURNAL Submitted (20-DEC-2000) Bioinformatics, ZymoGenetics, Inc., 1201  
Eastlake Ave. East, Seattle, WA 98102, USA  
FEATURES  
SOURCE Location/Qualifiers  
1..1710  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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/map="5p13-p12"  
1..1710  
/gene="CTR3"

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/note="ZACRP3"  
84..824  
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/db\_xref="GI:13274520"  
/translation="MIMROLIYVOLLAFPLPFCICODENYMSPTGSLPPDCSKCH  
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GVYFEFSMKHEDVEVYVILMHNGNTVFSYSEMKGSDTSSNBAVLKAKDEV  
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BASE COUNT 484 a 358 c 392 g 476 t  
ORIGIN

Alignment Scores:  
Pred. No.: 2.45e-96 Length: 1710  
Score: 1367.00 Matches: 246  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-036-041-2 (1-246) x AF329837 (1-1710)

QY 1 MetLeuTprArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPheLeuProPheCys 20  
DB 84 ATGCTTTGGAGGACCTCATCTATTGGCAACTGCTGCTTTTCTTCCCTTTTTC 143  
QY 21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40  
DB 144 CTGTCTCAAGATGATACATGATGATGATGATGATGATGATGATGATGATGATGAT 203  
QY 41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60  
DB 204 AAGCTTTCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 263  
QY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80  
DB 264 CCTCGCATTCACGAGAACCATGAGAACATGAGAACATGAGAACATGAGAACATGAGAAC 323  
QY 81 GlyAlaIleGlyGluGlyGlyAspIleGlyAspIleGlyProArgGlyGluArgGlyGln 100  
DB 324 GGAGCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 383  
QY 101 HisGlyProGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120  
DB 384 CATGGCCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 443  
QY 121 MetAlaSerIleuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140  
DB 444 ATGGCTTCTCTGCAACCCACTTCAGCAATCAGAACAGTGGGATTTCTTCACACACTGT 503  
QY 141 GluThrAsnIleGlyAsnPheAspValMetThrGlyArgPheGlyAlaProValSer 160  
DB 504 GAGACCAACATGGAACTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 563  
QY 161 GlyValIleTyrPhePheThrPheSerMetIleGlyAspValGluGluValTyrVal 180  
DB 564 GGTGTGATTTCTTACCTTCAGCATGAGACAGCATGAGGAGGAGGAGGAGGAGGAGGAG 623  
QY 181 TyrIleuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200  
DB 624 TACCTTATGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 683  
201 SerAspThrSerSerAsnHisAlaValIleuLysIleuAlaIleGlyAspGluValTyrPhe 220  
DB 684 TCAGATACATCCAGAACATGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 743  
QY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlyAsnArgPheSerThrPheAlaGlyPhe 240  
DB 744 CGAATGGCAATGGGCGCTCTCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 803

QY 241 LeuLeupheglurhrllys 246  
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 Db 804 CTGCTTTGAAACTAG 821

RESULT 4  
 AF326976 1730 bp mRNA linear PRI 03-JUL-2001  
 LOCUS AF326976  
 DEFINITION Homo sapiens putative secretory protein COR326 mRNA, complete cds.  
 ACCESSION AF326976  
 VERSION AF326976.1 GI:14586742  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Maeda,T., Hayashi,A. and Saito,T.  
 TITLE Molecular cloning, chromosomal localization, and genomic structure of the human COR326 gene  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1730)  
 AUTHORS Maeda,T.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-DEC-2000) Department of Radiology and Radiation  
 Oncology, Graduate School of Dentistry, Osaka University, 1-8  
 Yamadaoka, Suita, Osaka 565-0871, Japan  
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 1. 1730  
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 77. 817  
 /note="collagenous repeat-containing sequence"  
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 /protein\_id="AAK70344.1"  
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 /translation="MLRQLIWLQILFLPFLCQDEYMESPQGLPPDCSKCH  
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 PGEGKYPGIPPELOIAFMASLATHEFNONSGLIFSSVETNIGNFEDVMTGRGAPYS  
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 BASE COUNT 509 a 358 c 390 g 473 t  
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Alignment Scores:  
 Pred. No.: 2,48e-96 Length: 1730  
 Score: 1367.00 Matches: 246  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0

US-10-036-041-2 (1-246) x AF326976 (1-1730)

QY 1 MetLeuprpargrglnleuiletyrrtgrglnleuleualaleuphepheauprophecys 20  
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QY 21 LeuCySGLnaSpGLuYrMeTGLuSerProGlnThrGlyLeuProProAspCySser 40  
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 Db 137 CTGTGTCAAGATGATACATGAGAGTCTCCACAACCGAGAGACTACCCCAAGACTGCAGT 196

QY 41 LySCysyshtsGLysApTYrSerPheArgGLyTyrGlnGlnProProGlyProProGly 60  
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 Db 197 AAGTGTTCATGAGAGCTACAGCTTTTCGAGGCTACCAAGCCGCCCTTGAGCCACCGGGC 256

QY 61 ProProGlyLLeProGlyAsnHISGLYAsnAsnGlyAsnAsnGlyLalaTrnGlyHISGLu 80  
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 Db 257 CCTCTGCGCATTCAGAGAAACCATGGAACAATGAGCAACATGAGGACTGTCATGAA 316

QY 81 GlyAlaLysGLyGLuLysGLYAspLysGLYAspLysGLYProArgGLYGLuArgGLYGLu 100  
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 Db 317 GAGCCAAAGGTGAGAGGCGGACAAAGGTGACCTGGGGCTTCAGAGCGGAGCGGCAG 376

QY 101 HISGLYProLysGLYGLuLysGLYTYrProGlyLLeProProGlyLeuGlnLlalaPhe 120  
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 Db 377 CATGGCCCAAGAGAGAGAGAGGCGCTACCCGGGATTCACCAAGAACTTCAGATTGCATTC 436

QY 121 MetaLaserLeuAlaTrnHISpSerAsnGlnAsnSerGlyLlellePheSerSerVal 140  
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 Db 437 ATGCTCTCTGCGAACCCACTTCAGCAATGACAACAGTGGATTATCTTCAGCAGTCTT 496

QY 141 GLuThrAsnllleGlyAsnPheAspValMethTrGlyArgPheGlyAlaProValSer 160  
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 Db 497 GAGACCAACATGGAACACTTCTTGTATGTCATGACTGGTATATTGGGGCCCACTATCA 556

QY 161 GLYAlaTYrPhePheTrnPheSerMetMetLysHISGLYAspValGluGluValTYrVal 180  
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 Db 557 GGTTGTATTCTTCACCTTCACCATGATGAAAGATGAGATGGATTTATGTG 616

QY 181 TYrLeuMetHISAsnGlyAsnTrnValPheSerMetTYrSerTYrGluMetLysGLYlys 200  
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 Db 617 TACCTTATGCACATGCGAACACAGTCTTCAGCATGTACACTATGAAATGAAAGGCGCAA 676

QY 201 SerAspThrSerSerAsnHISAlaValleuLysLeuAlaLysGLYAspGLYAlaTrpleu 220  
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 Db 677 TCACATACATCCACCAACATCATGCTGCTGTAAGCTAGCCAAAGGGATGAGAGTTGGCTG 736

QY 221 ArgMetGLYAsnGlyAlaLeuHISGLYAspHISGlnArgPheSerTrnPhaLalGlyPhe 240  
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 Db 737 CGAATGGGCAATGGCGCTCTTCATGAGGACCAACACGCTTCTCCACCTTTCAGAGATTTC 796

QY 241 LeuLeupheglurhrllys 246  
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 Db 797 CTGCTTTGAAACTAG 814

RESULT 5  
 AX039955 1117 bp DNA linear PAR 18-NOV-2000  
 LOCUS AX039955  
 DEFINITION Sequence 11 from Patent WO0063377.  
 ACCESSION AX039955  
 VERSION AX039955.1 GI:11229976  
 KEYWORDS  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sclurognath; Muridae; Murinae; Mus.  
 REFERENCE  
 AUTHORS 1 (bases 1 to 1117)  
 TITLE Piddington,C.S. and Bishop,P.D.  
 JOURNAL Adipocyte complement related protein homolog zacrp3  
 Patent: WO 0063377-A 11 26-OCT-2000;  
 ZymoGenetics, Inc. (US)  
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 1. 1117  
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 BASE COUNT 284 a 272 c 293 g 268 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 3,14e-92 Length: 1117  
 Score: 1311.00 Matches: 236  
 Percent Similarity: 96.75% Conservative: 2





| QY | 161 | GLYVALTYRPHENPETHR-PHESERMETELCYSNHSIGLUAAPVALGLUVALTYRVAL    | 180 |
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| DB | 580 | GGTGGTATTTCTTCACCTTCAGCATGATGAAGACATGAGACGCTAGAGAACTGATGCG    | 639 |
| QY | 181 | TYRLEUMETHISASNGLYASNTHVALPHESERMETTYRSETTYGLUMELLYSLYLS      | 200 |
| DB | 640 | TACCTTATGACACAAAGGACACACACTCTTCAGCATGCTATGAAACAAAGGAAAA       | 699 |
| QY | 201 | SERASPTTRSERSEFASNHSIALVALLEULYLSLEUALALYSGLYASPCLVALTPLPU    | 220 |
| DB | 700 | TCAGTACATCCAGACACCATGCACTGCTGAGATTGGCCAAAGAGATGAGACTGGCTA     | 759 |
| QY | 221 | ARGMETGLYASNGLYALALEUHNISGLYASPHISGLINATRGPHSETRTHPHEALAGLPHE | 240 |
| DB | 760 | AGAATGGCCAAAGGAGCCCTCCAGCGGAGACACCAAGCGCTTCTCCACCTTGACAGCTTT  | 819 |
| QY | 241 | LEULEUPHEGLUPTHRLYS   | 246 |
| DB | 820 | CTGCTCTTTGAAACTAAG  | 837 |
| QY | 1   | MetLeuTRPARGLINLeuILeTYRTrpGLINLeuLeuAlaLeuPhePheLeuProPheCys | 20  |
| DB | 89  | ATGCTTTGAGAGACACCTCATGATGGAACAAGCTGGCTTTCTTTCTCCCTTTTGG       | 148 |
| QY | 21  | LeuCYSGlnAspGLUTyMetGLU                                       | 28  |
| DB | 149 | CTGTCTCAAGATGAATATCATGAGAGCGGAGACAACTAATAAGTGATGGCAAGAATA     | 208 |

|            |     |  |        |
|------------|-----|--|--------|
| QY         | 28  | -----  | 28     |
| Db         | 209 | GTGCAAGCCACCGACAGACTGGCCGTAGCGGCTTCAGAGGGAGAGAAGTAGAGACCGG         | 268    |
|            | 28  | -----  | 28     |
| Db         | 269 | AGCCATCCTAAACCTGGGACCTGTGATATATAACACTTCTACAGACCTAAATCCCTGAGA       | 328    |
| QY         | 28  | -----  | 28     |
| Db         | 329 | CCAGATGAGCTACCGCACCCGAGTAATGACTACAGCCAGATCACCAATTCCTGGGGC          | 388    |
| QY         | 29  | ---SerProGlnInThrGlyLeuProProAspGlySerSerGlyCysCysHisGlyAspTyr     | 47     |
| Db         | 389 | CAGTTCACCAACACCGGAGAGACTACCCCACTGCACATGATGTTGTCATGAGACACTAC        | 448    |
| QY         | 48  | SerPheArgGlyTyrGlyGlyProProGlyProProGlyProProGlyLleProGlyAsn       | 67     |
| Db         | 449 | AGCTTTCGAGGCTACCAAGGCCCCCTCTGGCCACCGGGCCCTCTCGGCAATTCAGGAAC        | 508    |
| QY         | 68  | HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlyGlyAlaLysGlyLysGly          | 87     |
| Db         | 509 | CATGAAACAATATGCGCAACATGAGACCCACTGTCATGAAGAGACCAAGAGTACAGAAAGGC     | 568    |
| QY         | 88  | AspLysGlyAspLeuGlyProArgGlyLysLysGlyGlnHisGlyProGlyGlyLys          | 107    |
| Db         | 569 | GACCAAGGTGACTCTGGGCTCTGAGGGAGCGGGGCGACAGATGGCCCAAGAGAGAGAG         | 628    |
| QY         | 108 | GlyTyrProGlyLleProProGlyLeuGlnIleAlaPheMetAlaSerLeuAlaThrHis       | 127    |
| Db         | 629 | GGCTACCGGGGATTCACACGAACCTTCAGATTGCATTTCATGGCTTCTCTGGCAACCCAC       | 688    |
| QY         | 128 | PheSerAsnGlnAsnSerGlyLleIlePheSerSerValGluThrAsnIleGlyAsnPhe       | 147    |
| Db         | 689 | TYCACCAATTCAGAACAGTGGGATTAATCTTCAGACACTGTTGAGACCACACATGGAAACTTC    | 748    |
| QY         | 148 | PheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPhe       | 167    |
| Db         | 749 | TT-GATGTCATGACTCGTGAATTTGGGGCCCCAGATACAGGTGTTATTCTTCACCTTC         | 807    |
| QY         | 168 | SerMetMetLysHisGlyAspValGluGlyAlaTyrValTyrLeuMetHisAsnGlyAsn       | 187    |
| Db         | 808 | AGCATGATGAAGACATGAGAGATTTGAGCAAGTGTATGTAACCTTATGCACATGGCAAC        | 867    |
| QY         | 188 | ThrValPheSerMetTyrSerTyrGluMetLysGlyLysSerAspThrSerSerHis          | 207    |
| Db         | 868 | ACAGCTTCACATGATACGATGTAATAATGAAGGCCAATAAGATACATCCACGACATATAT       | 927    |
| QY         | 208 | AlaValLleLysLysLeuAlaLysGlyAspGluValTyrPheLeuArgMetGlyAsnGlyAlaLeu | 227    |
| Db         | 928 | GCTGTGCTGAGACCTAGCCCAAGGGGATATAGCTTTGGCTCGCAATGGCGAATGGCGCTTC      | 987    |
| QY         | 228 | HisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPheGluThrLys          | 246    |
| Db         | 988 | CATGGGAGCACCAACACGCTCTCCACCTTTGCAGATTCCTGCTTGAACACTAG              | 1044   |
| RESULT 8   |     |  |        |
| AX136588   |     | 810 bp   | Linear |
| LOCUS      |     |  |        |
| DEFINITION |     | Sequence 510 from Patent EP1067182.                                |        |
| ACCESSION  |     | AX136588   |        |
| VERSION    |     | AX136588.1   |        |
| KEYWORDS   |     | GI:14272992  |        |
| SOURCE     |     | human.   |        |
| ORGANISM   |     | Homo sapiens   |        |
| REFERENCE  |     | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |        |
| AUTHORS    |     | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.        |        |
|            |     | Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and         |        |
|            |     | Hayashi,K.   |        |
| TITLE      |     | Secretory protein or membrane protein                              |        |
| JOURNAL    |     | Patent: EP 1067182-A 510 10-JAN-2001;                              |        |



| LOCUS                                      | AX191527   | 672 bp        | DNA | Linear | PAT 15-AUG-2001 |
|--|--|---------------|-----|--------|-----------------|
| DEFINITION                                 | Sequence 49 from Patent WO0149728.   |               |     |        |                 |
| ACCESSION                                  | AX191527   |               |     |        |                 |
| VERSION                                    | AX191527.1   | GI:15209709   |     |        |                 |
| KEYWORDS                                   |  |               |     |        |                 |
| SOURCE                                     | human.   |               |     |        |                 |
| ORGANISM                                   | Homo sapiens   |               |     |        |                 |
| REFERENCE                                  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;          |               |     |        |                 |
| AUTHORS                                    | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.                |               |     |        |                 |
| TITLE                                      | 1 (bases 1 to 672)   |               |     |        |                 |
| JOURNAL                                    | Kato, S. and Kimura, T.  |               |     |        |                 |
| FEATURES                                   | Human proteins having hydrophobic domains and dnas encoding these proteins |               |     |        |                 |
| source                                     | Patent: WO 0149728-A 49 12-JUL-2001;                                       |               |     |        |                 |
| BASE COUNT                                 | Protegene Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP)                 |               |     |        |                 |
| ORIGIN                                     | Location/Qualifiers  |               |     |        |                 |
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| DB:  | 6  | Gaps:         | 1   |        |                 |
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| OY   | 1 MetLeuTTParGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys              | 20            |     |        |                 |
| Db   | 1 ATGCTTTGGAGGACACCTCATATGGAACAGTGTGCTTTTCTCCTCCTTTTGC                     | 60            |     |        |                 |
| OY   | 21 LeuCysGlnAspGluTyrMetGlu  | 28            |     |        |                 |
| Db   | 61 CTGTGTCAGATGATATACATGAGGTGAGCGGAGAACATAAAGTGTGGCAAGATA                  | 120           |     |        |                 |
| OY   | 28   | 28            |     |        |                 |
| Db   | 121 GTGCAAGCCACACGACACTGCGCTGACCGGCTCCAGAGGGAGAGAAGTAGAGACGG               | 180           |     |        |                 |
| OY   | 28   | 28            |     |        |                 |
| Db   | 181 AGCCATCTTAACAACTGGGAGCTGTGATATAATAACAATTCTACAGACCTAAATCCCTGAGA         | 240           |     |        |                 |
| OY   | 28   | 28            |     |        |                 |
| Db   | 241 CCAGATGAGTACCGCACCCGAGGTAGATGACCTAGCCAGATCACCACATTCCTGGGCC             | 300           |     |        |                 |
| OY   | 29 ---SerProGlnThrGlyGlyLeuProProAspCysSerLeuCysHisGlyAspTyr               | 47            |     |        |                 |
| Db   | 301 CAGTCTCCACAAACCGGGAGACTACCCCAAGCTGCAAGTAAGTGTTCATGAGAGACTAC            | 360           |     |        |                 |
| OY   | 48 SerPheArgGlyTyrGlnGlyProProGlyProProGlyProProGlyLylLeuProGlyAsn         | 67            |     |        |                 |
| Db   | 361 AGCTTTCAGAGGTACCAAGGCCCCCTGGGACACCGGGGCCCTCTCGGCAATTCAGAGAAAC          | 420           |     |        |                 |
| OY   | 68 HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlyGlyAlaGlyGlyGlyGlyGlyGly         | 87            |     |        |                 |

| DB         | LOCUS    | DEFINITION   | ACCESSION | VERSION | KEYWORDS | SOURCE          | ORGANISM | REFERENCE | AUTHORS | TITLE | JOURNAL | REMARK | COMMENT |
|------------|----------|--|-----------|---------|----------|-----------------|----------|-----------|---------|-------|---------|--------|---------|
| DB         | 421      | CATGGAACCAATGGCAGACATGGACCCTGGTCTATGAAAGGACCAAGGTGAGAGAGGC   | 480       |         |          |                 |          |           |         |       |         |        |         |
| QY         | 88       | AsplysGlyAspLeuGlyProArgGlyGluArgGlyGlnHisGlyProGlyGlyGluGly | 107       |         |          |                 |          |           |         |       |         |        |         |
| DB         | 481      | GACAAAGGTGACCTGGGGGCTCGAGAGGAGCGGGGGGCGAGCATGGCCCAAGAGAGAAAG | 540       |         |          |                 |          |           |         |       |         |        |         |
| QY         | 108      | GlyTyrProGlyIleProProGluLeuGlnIleAlaPheMetAlaSerLeuAlaThrHis | 127       |         |          |                 |          |           |         |       |         |        |         |
| DB         | 541      | GGCTACCCGGGATTCACACAGACCTTCAGATTCAGATTCATGCTTCCTGGCAACCCAC   | 600       |         |          |                 |          |           |         |       |         |        |         |
| QY         | 128      | PheSerAsnGlnHisSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhe | 147       |         |          |                 |          |           |         |       |         |        |         |
| DB         | 601      | TTTACACATCAGACACAGTGGCATTTCTTCCACAGCTTTGACACCAACATTGGAACCTTC | 660       |         |          |                 |          |           |         |       |         |        |         |
| QY         | 148      | PheAspValMet   | 151       |         |          |                 |          |           |         |       |         |        |         |
| DB         | 661      | TTT-GATGTCATG  | 671       |         |          |                 |          |           |         |       |         |        |         |
| RESULT 11  | BC016021 | BC016021   | 1426 bp   | mRNA    | linear   | PRI 24-OCT-2001 |          |           |         |       |         |        |         |
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| REFERENCE  | BC016021 | BC016021   | 1426 bp   | mRNA    | linear   | PRI 24-OCT-2001 |          |           |         |       |         |        |         |
| AUTHORS    | BC016021 | BC016021   | 1426 bp   | mRNA    | linear   | PRI 24-OCT-2001 |          |           |         |       |         |        |         |
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| JOURNAL    | BC016021 | BC016021   | 1426 bp   | mRNA    | linear   | PRI 24-OCT-2001 |          |           |         |       |         |        |         |
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 BASE COUNT 446 a 264 c 278 g 438 t  
 ORIGIN

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US-10-036-041-2 (1-246) x BC016021 (1-1426)

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 DB 129 ATTCATTGATGAGCTTCCTGCAACCCATTCAGCAATCAGAAAGTGGATTATCTTC 188  
 OY 138 SerSerValGluThrAsnIleGlyAsnPhaPheAspValMetThrGlyArgPheGlyAla 157  
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 DB 189 AGCAGTGTGAGACCAACATTGAACTCTTGTGATGTCATGACTGTGATTTGGGGCC 248  
 OY 158 ProValSerGlyValTyrPhePheThrPheSerMetMetLysGluAspValGluGlu 177  
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 DB 249 CCAGTATCAGGTGTGATTTCTTCACCTTCAGCATGATGATGATGATGATGATGATG 308  
 OY 178 ValTyrValTyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMet 197  
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 DB 309 GTGATGTGATGATCTTATCAGCAATGCGCAACAGCTCTCAGCATGTACAGCTATGAAATG 368  
 OY 198 LysGlyLysSerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGlu 217  
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 DB 369 AAGGCAATATCAGTATCATCTTCAGCAATCATCTGCTGCAAGTCCGAGGGGATGAG 428  
 OY 218 ValTyrPheAsnGlyAsnGlyAlaLeuHisGlyAsnHisGlnArgPheSerThrPhe 237  
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 DB 429 GTTGGCGTGGCAATGGCAATGGCGCTCTCCATGGGAGCCACCAACGCTTCTCCACCTTT 488  
 OY 238 AlaGlyPheLeuLeuPheGluThrLys 246  
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 DB 489 GCAGGATTCCTGCTCTTGAACATAAG 515

## RESULT 12

LOCUS AX079496 546 bp DNA linear PAT 22-FEB-2001  
 DEFINITION Sequence 240 from Patent WO0107611.  
 ACCESSION AX079496  
 VERSION AX079496.1 GI:13159056  
 KEYWORDS

## SOURCE

human.

## ORGANISM

Homo sapiens

## REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

## AUTHORS

Baker, K.P., Goddard, A. and Wood, M.I.

## TITLE

Human polypeptides and methods for the use thereof

## JOURNAL

Patent: WO 0107611-A 240 01-FEB-2001;

## FEATURES

Location/Qualifiers

## source

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 /db\_xref="taxon:9606"

## BASE COUNT

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## ORIGIN

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US-10-036-041-2 (1-246) x AX079496 (1-546)

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 DB 397 AGCTTTCAGAGCTACCAAGGCCCCCTGGGCGGCGGCGCTCTGCGCATTCAGAGAAAC 456  
 OY 68 HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGluGlyAlaLysGlyGluLysGly 87  
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## RESULT 13

LOCUS AX054802 912 bp DNA linear PAT 13-JAN-2001  
 DEFINITION Sequence 1 from Patent WO0073448.  
 ACCESSION AX054802  
 VERSION AX054802.1 GI:12228257  
 KEYWORDS

## SOURCE

human.

## ORGANISM

Homo sapiens

## REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

## AUTHORS

Piddington, C.S. and Sheppard, P.O.

## TITLE

Adipocyte complement related protein homolog zacr7

## JOURNAL

Patent: WO 0073448-A 1 07-DEC-2000;

## FEATURES

Location/Qualifiers

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## CDS

1..912  
 /note="unnamed protein product"

## ORIGIN

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RESULT 15
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DEFINITION Homo sapiens, complement-clq tumor necrosis factor-related protein
ACCESSION BC022187
VERSION BC022187.1 GI:18381162
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
COMMENT NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
Contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahney, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

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Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAC Plate: 33 Row: k Column: 8  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: GenomeScan gene  
 prediction, similarity but not identity to protein.

#### FEATURES

Location/Qualifiers

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BASE COUNT 1242 a 758 c 874 g 1085 t  
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US-10-036-041-2 (1-246) x BC022187 (1-3959)

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Db 534 GCGAAGAAAGAGACCCATGAGACAGAGAGAGAGAAAGAGATGATGTCATTTGGTCTCT 593
Oy 104 -----LysGlyGluLysGlyTyrProGlyIleProPro----- 114
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QY 188 ThrValPheSerMetTyrSerTyrGluMetLys-----GlyLysSer 201
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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Run on: January 15, 2003, 19:40:50 ; Search time 2237 Seconds

(without alignments)  
1780.997 Million cell updates/sec

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Perfect score: 1367

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Fgapop 6.0, Fgapext 7.0  
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Searched: 16154066 seqs, 8097743376 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=EST -QPM=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -STRAT=1 -END=1 -MATRIX=blissum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTEWT=plc -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10036041@cgn.1.1716@runat.13012003.160809.7069 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120  
-NARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: em\_estdb:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_Other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Match | Length | DB | ID       | Description        |
|------------|--------|-------|--------|----|----------|--------------------|
| 1          | 1238.5 | 90.6  | 1103   | 14 | BM924169 | BM924169 AGENCOURT |
| 2          | 1153   | 84.3  | 815    | 13 | B1757458 | B1757458 603029396 |
| 3          | 1137.5 | 83.2  | 1007   | 14 | B0958105 | B0958105 AGENCOURT |
| 4          | 1093   | 80.0  | 724    | 9  | A1956432 | A1956432 u127p06.y |
| 5          | 1065   | 77.9  | 636    | 14 | B0637986 | B0637986 hdl7a10.y |
| 6          | 1035   | 75.7  | 692    | 9  | A1006567 | A1006567 ue1408.y  |
| 7          | 995.5  | 72.8  | 680    | 9  | A1527737 | A1527737 u128e09.y |
| 8          | 994    | 72.7  | 631    | 12 | BF788496 | BF788496 602114255 |
| 9          | 992    | 72.6  | 631    | 12 | BF784596 | BF784596 602110304 |
| 10         | 958    | 70.1  | 656    | 10 | AM318621 | AM318621 un02e01.y |
| 11         | 953    | 69.7  | 635    | 10 | BB572119 | BB572119 BB572119  |
| 12         | 934    | 68.3  | 703    | 10 | BB649178 | BB649178 BB649178  |
| 13         | 909    | 66.5  | 662    | 10 | BB610546 | BB610546 BB610546  |
| 14         | 820.5  | 60.0  | 571    | 9  | A1316916 | A1316916 u124c04.y |
| 15         | 793    | 58.0  | 828    | 12 | BG400260 | BG400260 602464652 |
| 16         | 764.5  | 55.9  | 687    | 13 | B1143591 | B1143591 602907423 |
| 17         | 741    | 54.2  | 525    | 12 | BF924264 | BF924264 MR2-NT013 |
| 18         | 733    | 53.6  | 475    | 9  | A1430561 | A1430561 md89a11.y |
| 19         | 727    | 53.2  | 553    | 9  | AA821459 | AA821459 vs25g06.x |
| 20         | 721    | 52.7  | 413    | 9  | A1892360 | A1892360 mm59g11.y |
| 21         | 717    | 52.5  | 413    | 9  | A1325676 | A1325676 mm59g11.y |
| 22         | 715    | 52.3  | 412    | 9  | AA068843 | AA068843 mm59g11.y |
| 23         | 689    | 50.4  | 508    | 10 | BB867706 | BB867706 BB867706  |
| 24         | 677    | 49.5  | 762    | 12 | BG201468 | BG201468 RST20685  |
| 25         | 677    | 49.5  | 770    | 12 | BG195757 | BG195757 RST14951  |
| 26         | 677    | 49.5  | 773    | 12 | BG204962 | BG204962 RST24381  |
| 27         | 672    | 49.2  | 776    | 12 | BG186424 | BG186424 RST5388.A |
| 28         | 669    | 48.9  | 794    | 12 | BG571867 | BG571867 602593213 |
| 29         | 669    | 48.9  | 804    | 12 | BG203434 | BG203434 RST22817  |
| 30         | 646    | 47.3  | 474    | 9  | AA637749 | AA637749 vt29c01.r |
| 31         | 643    | 47.0  | 464    | 10 | AA318481 | AA318481 um97f05.y |
| 32         | 639    | 46.7  | 803    | 12 | BG228003 | BG228003 RST41923  |
| 33         | 633    | 46.3  | 780    | 12 | BG199309 | BG199309 RST18591  |
| 34         | 629    | 46.0  | 355    | 9  | AA334609 | AA334609 EST38850  |
| 35         | 629    | 46.0  | 577    | 10 | AV597266 | AV597266 AV597266  |
| 36         | 620    | 45.4  | 536    | 14 | R61190   | R61190 yH06b10.r1  |
| 37         | 568    | 41.6  | 341    | 9  | AA322403 | AA322403 EST25036  |
| 38         | 546    | 39.9  | 529    | 9  | AA224157 | AA224157 zt14f03.x |
| 39         | 521    | 38.1  | 294    | 9  | AA332783 | AA332783 EST36794  |
| 40         | 513    | 37.5  | 299    | 12 | BG195755 | BG195755 RST14949  |
| 41         | 453.5  | 33.2  | 610    | 9  | A1317686 | A1317686 u122d04.y |
| 42         | 429.5  | 31.4  | 513    | 12 | BG202375 | BG202375 RST21732  |
| 43         | 411    | 30.1  | 540    | 13 | B1964193 | B1964193 i66a10.y  |
| 44         | 411    | 30.1  | 555    | 13 | B1964101 | B1964101 i66a10.y  |
| 45         | 410    | 30.0  | 369    | 14 | W64775   | W64775 md89a11.r1  |

#### ALIGNMENTS

RESULT 1  
BM924169  
LOCUS BM924169 1103 bp mRNA linear EST 12-MAR-2002  
DEFINITION AGENCOURT.6630525 NIH\_MGC\_116 Homo sapiens CDNA clone IMAGE:5760396  
5', mRNA sequence.  
ACCESSION BM924169  
VERSION BM924169.1 GI:19374548  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1103)  
NIH-MGC http://mgi.mc.nhl.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE



Query Match: 84.35% Indels: 7  
DB: 13 Gaps: 0

US-10-036-041-2 (1-246) x B1757458 (1-815)

3 TTPARGINLEU1ETRTTPTG1NLEU1ALEUPHLEUPROPHCYSLCYC 22  
|||||  
20 TGGAGGAGCTCATCTATTGGCAACGCTGCTTGTCTGCT-CCCTTTTGGCTGTCT 77  
|||||

23 G1NAPSPLUTYMETGLUSERPROGINTHGLVLEUPROPROA5CYSSERLYSCYS 42  
|||||

78 CAGATGATATACATGAGGTCTCCACAAACCGAGAGACTACCCGAGACTGCAGTAAGTG- 136  
|||||

43 CYSHISGLVSPRYTSERPHETATGGLTYTGTGLNGLYPROPROGLYPROPROGLYPROPRO 62  
|||||

137 TGTCAATGGAACACACACTTTCAGAGGCTACCAAGGCCCTGGGCCACCGGGCTCTCT 196  
|||||

63 G1Y1LEPROGLVSNHISGLVSNASNGLYASNANGLVALATHRGLVHISGLVLA 82  
|||||

197 GGCATTTCCAGAAACCATGGAAACATGGCAACATGAGCCACTGGTCAATGAAGACC 256  
|||||

83 LYSGLVGLUTYSGLYASPLYSGLVSPLEUGLYPROARGLYGUATRGLYLNHISGLY 102  
|||||

257 AAGGTGAGAAAGGCGCAAAAGGTGACCTGGGGCTCGAGGGGAGCGGGGACACCTAGGC 316  
|||||

103 PROLYSGLYGLUTYSGLYTTPROGLY1LEPROPROGLYUENGLINLEAPHEMETA 122  
|||||

317 CCCAAGAGAGAGAGGCTACCGGGGATTCACACAGACTTCAGATTGCAATCATGGCT 376  
|||||

123 SERLEU1ATHRHISPHESERASNG1ASNSEGLY1LE1LEPHESERVALGLUTHR 142  
|||||

377 TCTCTGGCAACCCACTTCACACATGACAGACAGTGGATTCTTCACAGCTGGTGAACCC 436  
|||||

143 ASN1LEGLVSNRPHESPVALMETLTHGLVARGPHEGLVALAPROVALSERGLVVAL 162  
|||||

437 AACATTGGAACCTCTTGTGATGCATGACTGGTGGATTGGGGCCAGATTCAGGTG 496  
|||||

163 TYRPHETHRPHESERMETLTHSGLVSNVALGLUGLVALTYRVALTYRLEU 182  
|||||

497 TATTTCTTCACTTCACAGATGATGACATGAGATGTTGGAGAGTATGTACTCTT 556  
|||||

183 METHASNG1ASNTRVALPHESERMETLTHSERTYRGLUMETLTHSGLVLYSERASP 202  
|||||

557 ATGCACATGGCACAACAGCTTTCAGCATGACGCTATGAATGAAGGCAATTCAGAT 616  
|||||

203 THRSERASN1SALVALLEU-LYSLEUALA-LYSGLVSPGLVALTYRPLEUARGM 222  
|||||

617 ACATCCAGCATCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 675  
|||||

222 ECLVSNGLVALALEU1HISGLVSPHISGLVSNHISGLVSNHISGLVSNHISGLV 242  
|||||

676 TGGCAATGGGCTCTCCATGAGGGA-CACCAACGCTTCTCCAC-TTTCAGAGATTCTGCT 733  
|||||

242 EUPHETGLUTHTLVS 246  
|||||

734 CTTTGAACCTAAG 747  
|||||

RESULT 3  
B0958105 1007 bp mRNA linear EST 21-AUG-2002  
LOCUS B0958105  
DEFINITION ACENCOUR1\_10013971 NCI\_CGAP\_Mam2 Mus musculus cDNA clone  
IMAGE:6486507 5', mRNA sequence.  
ACCESSION B0958105  
VERSION B0958105.1 GI:22373583  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1007)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LLM14030 row: a column: 04  
High quality sequence stop: 622.  
Location/Qualifiers  
1. 1007  
/organism="Mus musculus"  
/strain="FVB/N-3"  
/db\_xref="taxon:10090"  
/clone="IMAGE:6486507"  
/clone\_1lb="NCI\_CGAP\_Mam2"  
/tissue\_type="tumor, biopsy sample"  
/dev\_stage="5 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Salt;  
Site: 2; Note: Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"

BASE COUNT 253 a 236 c 280 g 231 t 7 others  
ORIGIN

Alignment Scores:  
Pred. No.: 3.65e-101 Length: 1007  
Score: 1137.50 Matches: 216  
Percent Similarity: 87.70% Conservative: 5  
Best Local Similarity: 85.71% Mismatches: 21  
Query Match: 83.21% Indels: 10  
DB: 14 Gaps: 5

US-10-036-041-2 (1-246) x B0958105 (1-1007)

1 METLEUTPARGLINLEU1ETRTTPTG1NLEU1ALEUPHLEUPROPHCYC 20  
|||||

95 ATGCTCGGAGAGCAGCGCATGTGGTGCCACTGCTGCTTGTCTTCTCCATTTTGC 154  
|||||

21 LEUCYSG1NAPSGLUTYMETGLUSERPROGINTHRGLVLEUPROPROA5CYSSER 40  
|||||

155 CTGTCTCAAGATGATGATGAGCTCCACAGCTGGAGAGACTGCCCAAGCTGCAGC 214  
|||||

41 LYSCTCYSHISGLVSPRYTSERPHETATGGLTYTGTGLNGLYPROPROGLYPROPROGLY 60  
|||||

215 AAGTGTCCCATGCAATGATGATGATTTGTGCTTCCAAAGGCCCCCTGGAGCTCAGCT 274  
|||||

61 PROPROGLY1LEPROGLVSNHISGLVSNANGLVSNANGLVALATHRGLVHISGLU 80  
|||||

275 CCTCTGCGCATTCAGAAACCATGAGAAACATGAGAAACATGAGAAACATGAGAAAC 334  
|||||

81 GLVALALYSGLVGLUTYSGLYASPLYSGLVSPLEUGLYPROARGLYGUATRGLYLN 100  
|||||

335 GGGGCCAAAGGTGAGAAAGAGACAAAGCGCCCTGAGGAGAACGGGGGAG 394  
|||||

101 H1SGLYPROLYSGLYGLUTYSGLYTTPROGLY1LEPROPROGLYUENGLINLEAPHE 120  
|||||

395 CATGGCCCCAAGAGAGAAAGCTACCCAGGGGTGCCACCAAGCTCAGATTGCTATTC 454  
|||||

121 METALASERLEUALATHRHISPHESERASNG1ASNSEGLY1LE1LEPHESERVAL 140  
|||||

455 ATGCTCTTCTAGCAACATCTTCAGCAATGAGACATGAGATGATATCTTCAGCAGTGT 514  
|||||

141 GLUTHRASN1LEGLVSNRPHESPVALMETLTHRGLVARGPHEGLVALAPROVALSER 160  
|||||

515 GAGACCAACATTTGGAACCTTTCATGATGATGAGAGATTTGGGGCCCCCTATCA 574  
|||||

161 GLVATYRPHETHRPHESERMETLTHSGLVSNVAL-GLUGLVALTYRVA 180  
|||||

575 GGTGTGATTTCTTCACTTTCAGCATGATGAACATGAGAGAGCTNAGAGGAAGTATGT 634  
|||||

QY 180 1TYrLeMeHIsAnGlyAsnThrValPheSerMetTySerTyrGluMetLysGly 200  
 Db 635 GTACCTTATGCACACGCGACACAGCTTCACATGTACATGACAAAGGAAA 694  
 QY 200 sSerAspThrSerSerAsnHisAlaValLeuLysLeuAla--LysGlyAspGluValTr 219  
 Db 695 ATCAGATACATCCAGCATGNCAGNCTGCTGAAGTTGGCCAAAGAGAGATGACATGCTG 754  
 QY 219 pLeuArgMeGlyAsnGlyAlaLeu-----HisGlyAspHisGlnArg--Ph 234  
 Db 755 GGCTAG-----AATGGGCGACAGNGTGGCCCTCCACAGNGGAGCCACACGCGCTTCT 808  
 QY 234 eSerThrPheAlaGly---PheLeuLeuPheGlu 244  
 Db 809 TCACCTTTCGACGCGCTTTCCTCTTTTGA 842

RESULT 4  
 A1956432 724 bp mRNA linear EST 20-AUG-1999  
 LOCUS ul77b06.y1 Sugano mouse kidney mklia Mus musculus cDNA clone  
 DEFINITION IMAGE:2136563 5' similar to SW:CERL\_RAT P98087 CEREBELLIN-LIKE  
 GLYCOPROTEIN. ; mRNA sequence.

ACCESSION A1956432  
 VERSION A1956432  
 KEYWORDS GI:5749141  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE Eukaryota: Chordata: Craniata: Vertebrata: Euteleostomi:  
 Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.  
 1 (bases 1 to 724)  
 AUTHORS Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
 Underwood, K., Steple, M., Theising, B., Allen, N., Bowers, Y., Person,  
 B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter,  
 E., Kohn, S., Shun, T., Jackson, F., Cardenas, M., McCann, R.,  
 Waterston, R. and Wilson, R.  
 The WashU-NCI Mouse EST Project 1999  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Maria M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.wustl.edu  
 This clone is available royalty-free through INM: contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 MGI:1001239

FEATURES  
 source  
 Possible reversed clone: similarity on wrong strand  
 Seg primer: custom primer used  
 High quality sequence stop: 511.  
 Location/Qualifiers  
 1..724

/organism="Mus musculus"  
 /strain="C57BL"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:2136563"  
 /clone\_lib="Sugano mouse kidney mklia"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Organ: kidney; Vector: pME18S-FL3; Site:1: DraIII  
 (CACTGTGTG); Site:2: DraIII (CACCATGTG); 1st strand cDNA  
 was primed with an oligo(dT) primer  
 (ATGCGCCCTTTTCTTTTCTTTT); double-stranded cDNA was  
 ligated to a DraIII adaptor (TTTGGCCCTACTGG), digested  
 and cloned into distinct draIII sites of the pME18S-FL3  
 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should  
 be used to isolate the cDNA insert. Size selection was  
 performed to exclude fragments <1.5kb. Library  
 constructed by Dr. Sumio Sugano (University of Tokyo  
 Institute of Medical Science). Custom primers for  
 sequencing: 5' end primer CTCTCTCTCTTAAAGACTGCG and 3' end  
 primer CGACCTCGACGCTCGAGCACA."

BASE COUNT 185 a 187 c 190 g 159 t 3 others  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 5.76e-97 Length: 724  
 Score: 1093.00 Matches: 196  
 Percent Similarity: 94.76% Conservative: 3  
 Best Local Similarity: 93.33% Mismatches: 11  
 Query Match: 79.96% Indels: 0  
 Ds: 9 Gaps: 0  
 US-10-036-041-2 (1-246) x A1956432 (1-724)  
 QY 1 MetLeuTrpArgGlnLeuLeuIleTyrTrpGlnLeuLeuAlaLeuPheLeuPropheCys 20  
 Db 95 ATGCTGGGAGGCGACGCATCTGTGTGACCTCTGCTTCTTCTTCTCCATTTTGC 154  
 QY 21 LeuCySglnAspGluTyrMetGlnSerProGlnThrGlyLeuPropProAspCysSer 40  
 Db 155 CTGTGCAAGATTAATACATGAGTCTCCCAAGCTGAGAGACTGCCGCCAGACTGCAGC 214  
 QY 41 LysCySglnHisGlyAspTyrSerPheAlaGlyTyrGlnGlyProProGlyProProGly 60  
 Db 215 AACTGTGGCCATGAGATTAATGATTTCGTGTACCAAGGCCCTGGACCTCCAGGT 274  
 QY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAlaThrGlyHisGlu 80  
 Db 275 CTTCTGGCATTTCCAGGAACATGCAACATGCGACATGACCTACTGCGCATGAA 334  
 QY 81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100  
 Db 335 GGGGCCAAAGGTGAGAAGAAGAGCAAAAGGCGACCTAGGCGCTCGAGAGAAAGCGGCGAG 394  
 QY 101 HisGlyProLysGlyLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120  
 Db 395 CAGGCGCCCAAGAGAGAGAAAGGCTACCAAGGGGTGCCACCAACATGCGCATTTGCATTC 454  
 QY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140  
 Db 455 ATGGCTTCTTACCACTACTCTTACCAATCAGAACAGTGGCATTTATCTTCACAGCTTT 514  
 QY 141 GluThrAsnIleGlyAsnPheAspValMetThrGlyArgPheGlyAlaProValSer 160  
 Db 515 GAGACCAACATTTGAAACTCTTCGATGATCATCATGNGAGATTGGGCCCGGTATCA 574  
 QY 161 GlyValTyrPhePheThrPheSerMetMetLysHisGlnAspValGluGluValTyrVal 180  
 Db 575 GGGTGTATTTCTTCACTTACCATGATGAAACATGAGACCTAGAGAAAGTGTATGTG 634  
 QY 181 TYrLeMeHIsAnGlyAsnThrValPheSerMetTySerTyrGluMetLysGlyLys 200  
 Db 635 TACCTTATGCACACGCGCAACAGCTTCACATGTACATGACAAAGGAAA 694  
 QY 201 sSerAspThrSerSerAsnHisAlaValLeu 210  
 Db 695 TCAGATACATCCAGCAACCATGAGTGTG 724  
 RESULT 5  
 LOCUS B0637986 636 bp mRNA linear EST 15-JUL-2002  
 DEFINITION hd17a10.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he  
 Homo sapiens cDNA clone hd17a10 5', mRNA sequence.  
 ACCESSION B0637986  
 VERSION B0637986.1 GI:21762445  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota: Chordata: Craniata: Vertebrata: Euteleostomi:  
 Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo.  
 1 (bases 1 to 636)  
 AUTHORS Wistow, G., Bernstein, S.L., Wyatt, M.K., Ray, S., Behal, A., Touchman  
 J.W., Bouffard, G., Smith, D. and Peterson, K.  
 Expressed sequence tag analysis of human retina for the NEIBank



|                        |               |        |
|------------------------|---------------|--------|
| Pred. No.:             | 2             | 57e-91 |
| Score:                 | 1035          | 00     |
| Percent Similarity:    | 95            | .88%   |
| Best Local Similarity: | 94            | .65%   |
| Query Match:           | 75            | .71%   |
| DB:                    | 9             |        |
|                        |               |        |
|                        | length:       | 6522   |
|                        | Matches:      | 1840   |
|                        | Conservative: | 2      |
|                        | Mismatches:   | 8      |
|                        | Indels:       | 0      |
|                        | Gaps:         | 0      |

| Y                      | 141  | GIUThrAsn1IeGlyAsnPhpheAspValMetThnGlyArgPheGlyAlaProValSer     | 160 |
|------------------------|--|---|-----|
| Db                     | 478  | -----   | 478 |
| QY                     | 161  | GlyValTyrPhePheThrPheSerMetGlySHISGLuAspValGluGluValTyrVal      | 180 |
| Db                     | 479  | -----TTGAGCATGATGAAAGCATGAGACAGTGAAGAGCATGTATG                  | 520 |
| QY                     | 181  | TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys    | 200 |
| Db                     | 521  | TACCTTAGTCACAAACGCGAACACACTCTTCACACATGTACAGCTATGAAACAAGGAGAAAA  | 580 |
| QY                     | 201  | SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaAlaGlyAspGluValTyrPheLeu | 220 |
| Db                     | 561  | TCAGATACATCCAGCAACCATCATGCGCTGGAAGTGGCCAAAGAGATAGATGCTGGCTA     | 640 |
| QY                     | 221  | ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArg                         | 233 |
| Db                     | 641  | AGAAATGGCAACGATGCGCTCCACGGNAGNACCAACGAGCG                       | 679 |
| RESULT 8               |  |   |     |
| BF788496               |  |   |     |
| LOCUS                  | 602114255P1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4242612   | 631 bp . mRNA linear EST 12-JAN-2001                            |     |
| DEFINITION             | 5', mRNA sequence.   |   |     |
| ACCESSION              | BF788496   |   |     |
| VERSION                | BF788496.1 GI:12093532   |   |     |
| KEYWORDS               | EST.   |   |     |
| SOURCE                 | house mouse.   |   |     |
| ORGANISM               | Mus musculus   |   |     |
| REFERENCE              | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |   |     |
| AUTHORS                | 1 (bases 1 to 631)   |   |     |
| TITLE                  | NIH-MGC http://mgc.nci.nih.gov/.   |   |     |
| JOURNAL                | National Institutes of Health, Mammalian Gene Collection (MGC)   |   |     |
| COMMENT                | Unpublished (1999)   |   |     |
|                        | Contact: Robert Strausberg, Ph.D.  |   |     |
|                        | Email: cgapbs-remail.nih.gov   |   |     |
|                        | Tissue Procurement: Jeffrey E. Green, M.D.   |   |     |
|                        | cDNA Library Preparation: Life Technologies, Inc.  |   |     |
|                        | CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  |   |     |
|                        | DNA Sequencing by: Incyte Genomics, Inc.   |   |     |
|                        | Clone distribution: MGC clone distribution information can be  |   |     |
|                        | found through the I.M.A.G.E. Consortium/LLNL at:   |   |     |
|                        | http://image.llnl.gov  |   |     |
|                        | Plate: LHM9860 row: m column: 13   |   |     |
|                        | High quality sequence stop: 623.   |   |     |
| FEATURES               |  |   |     |
| Source                 | Location/Qualifiers  |   |     |
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|                        | /organism="Mus musculus"   |   |     |
|                        | /strain="FVB/N"  |   |     |
|                        | /db_xref="taxon:10090"   |   |     |
|                        | /clone="IMAGE:4242612"   |   |     |
|                        | /clone_lib="NCI CGAP_Kid14"  |   |     |
|                        | /lab_host="DH10B (TI phage-resistant)"   |   |     |
|                        | /note="Organ: Kidney; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.                    |   |     |
|                        | Average insert size 1.75 kb. Constructed by Life   |   |     |
|                        | Technologies. Note: this is a NCI_CGAP Library.  "   |   |     |
| BASE COUNT             | 181 a 154 c 176 g 120 t  |   |     |
| ORIGIN                 |  |   |     |
| Alignment Scores:      |  |   |     |
| Pred. NO.:             | 2.38e-87   | Length:   | 631 |
| Score:                 | 994.00   | Matches:  | 193 |
| Percent Similarity:    | 96.06%   | Conservative:   | 2   |
| Best Local Similarity: | 95.07%   | Mismatches:   | 8   |
| Query Match:           | 72.71%   | Indels:   | 4   |
| DB:                    | 12   | Gaps:   | 0   |
| Y                      | 28   | GIUSePrroGInThnGlyGlyLeuProPdaPcySserLysCysCysHisGlyAspTyr      | 47  |

| QY | Db | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 | 101 | 102 | 103 | 104 | 105 | 106 | 107 | 108 | 109 | 110 | 111 | 112 | 113 | 114 | 115 | 116 | 117 | 118 | 119 | 120 | 121 | 122 | 123 | 124 | 125 | 126 | 127 | 128 | 129 | 130 | 131 | 132 | 133 | 134 | 135 | 136 | 137 | 138 | 139 | 140 | 141 | 142 | 143 | 144 | 145 | 146 | 147 | 148 | 149 | 150 | 151 | 152 | 153 | 154 | 155 | 156 | 157 | 158 | 159 | 160 | 161 | 162 | 163 | 164 | 165 | 166 | 167 | 168 | 169 | 170 | 171 | 172 | 173 | 174 | 175 | 176 | 177 | 178 | 179 | 180 | 181 | 182 | 183 | 184 | 185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200 | 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300 | 301 | 302 | 303 | 304 | 305 | 306 | 307 | 308 | 309 | 310 | 311 | 312 | 313 | 314 | 315 | 316 | 317 | 318 | 319 | 320 | 321 | 322 | 323 | 324 | 325 | 326 | 327 | 328 | 329 | 330 | 331 | 332 | 333 | 334 | 335 | 336 | 337 | 338 | 339 | 340 | 341 | 342 | 343 | 344 | 345 | 346 | 347 | 348 | 349 | 350 | 351 | 352 | 353 | 354 | 355 | 356 | 357 | 358 | 359 | 360 | 361 | 362 | 363 | 364 | 365 | 366 | 367 | 368 | 369 | 370 | 371 | 372 | 373 | 374 | 375 | 376 | 377 | 378 | 379 | 380 | 381 | 382 | 383 | 384 | 385 | 386 | 387 | 388 | 389 | 390 | 391 | 392 | 393 | 394 | 395 | 396 | 397 | 398 | 399 | 400 | 401 | 402 | 403 | 404 | 405 | 406 | 407 | 408 | 409 | 410 | 411 | 412 | 413 | 414 | 415 | 416 | 417 | 418 | 419 | 420 | 421 | 422 | 423 | 424 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 441 | 442 | 443 | 444 | 445 | 446 | 447 | 448 | 449 | 450 | 451 | 452 | 453 | 454 | 455 | 456 | 457 | 458 | 459 | 460 | 461 | 462 | 463 | 464 | 465 | 466 | 467 | 468 | 469 | 470 | 471 | 472 | 473 | 474 | 475 | 476 | 477 | 478 | 479 | 480 | 481 | 482 | 483 | 484 | 485 | 486 | 487 | 488 | 489 | 490 | 491 | 492 | 493 | 494 | 495 | 496 | 497 | 498 | 499 | 500 | 501 | 502 | 503 | 504 | 505 | 506 | 507 | 508 | 509 | 510 | 511 | 512 | 513 | 514 | 515 | 516 | 517 | 518 | 519 | 520 | 521 | 522 | 5 |
|----|----|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|
|----|----|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|



|  |  |
|--|--|
| REFERENCE                                  | Makaryova; Metzros; Chordata; Craniata; Vertebrata; Euteleostomi;  |
| AUTHORS                                    | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.   |
| JOURNAL                                    | 1 (bases 1 to 656)   |
| TITLE                                      | Maria,M., Hillier,L., Kucab,T., Martin,J., Beck,C., Wylie,T.,<br>underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,<br>.B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,<br>.E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,<br>Waterston,R. and Wilson,R.<br>The WashU-NCI Mouse EST Project 1999<br>Unpublished (1999)<br>Other ESTs: un02e01.x1<br>Contact: Maria M/WashU-NCI Mouse EST Project 1999<br>Washington University School of Medicine<br>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA<br>Tel: 314 286 1800<br>Fax: 314 286 1810<br>Email: mouseest@watson.wustl.edu<br>This clone is available royalty-free through LNL ; contact the<br>IMAGE Consortium ( <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> ) for further information.<br>MGI:1012316<br>Seq primer: custom primer used<br>High quality sequence stop: 449.                      |
| FEATURES                                   | Location/Qualifiers  |
| SOURCE                                     | 1..656<br>/organism="Mus musculus"<br>/strain="C57BL/<br>/db_xref="taxon:10090"<br>/clone="IMAGE:2372664"<br>/clone_lib="Sugano mouse kidney mktia"<br>/sex="female"<br>/dev_stage="adult"<br>/lab_host="DH10B"<br>/note="Organ: kidney; Vector: pME18S-FL3; Site:1: DraIII<br>(CACCTGCG); Site:2: DraIII (CACCAATGG); 1st strand cDNA<br>was primed with an oligo(dT) primer<br>[ATGGGCCCTTTTTCCTTTTTTTT]; double-stranded cDNA was<br>ligated to a DraIII adaptor (tttggcgctactgc), digested<br>and cloned into distinct DraIII sites of the pME18S-FL3<br>vector (5' site CACTGTGT, 3' site CACCAATGG). XhoI should<br>be used to isolate the cDNA insert. Size selection was<br>performed to exclude fragments <1.5kb. Library<br>constructed by Dr. Sumio Sugano (University of Tokyo<br>Institute of Medical Science). Custom primers for<br>sequencing: 5' end primer CTTCGCTCTAAAGCTCCG and 3' end<br>primer GCACCTGCAGCTCAGCA." |
| BASE COUNT                                 | 177 a 172 c 156 g 146 t 5 others   |
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| Pred. No.:                                 | 8..21e-84 Length: 656  |
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| DB:  | Gaps: 0  |
| US-10-036-041-2 (1-246) x AW318621 (1-656) |  |
| OY 1                                       | MelLeuTPPARGlnLeuLeuLeuTYrrpgLnLeuAlaLeuPhenProPhecys 20   |
| Db 78                                      | ATGCTCGGGAGGAGCGCATGTGGTGACCCTGCGCTTCCTTCCTCCATTTCGC 137   |
| OY 21                                      | LencuSglnaspGluIuryrmetGiuserPROGINTHnglglyLleuProPAscysSer 40   |
| Db 138                                     | CTGTGTCAAGATAATACATGAGTGTCCACCAAGCTGGAGGAGCTCCCCAGACTGGAGC 197   |
| OY 41                                      | LyscysCSyHslsglyasPTyrSerPhearqglTYrrgInglyProProglyProProgly 60   |
| Db 198                                     | AAGGTTCGCCATGAGAATTATGATTTGCTGTGTTACCAAGGCCCCCCTGGACCTCCAGGT 257   |
| OY 61                                      | ProProglyLyleProglyasnHslsglyasnasnnglyasnasnnglyalaThrhglyHslgu 80  |
| Db 258                                     | CCTTCGCGCATTCACGAACAACATGGAAAACAATGGAACAAATGGAGCTACAGCCATGAA 317   |



|            |  |  |        |
|------------|--|--|--------|
| Db         | 340  | GGGGCAAGAGTGTGAAAGAGACAAAGCGACCTGAGCCCTCGAGAGAAAGCGGGCAG     | 399    |
| Qy         | 101  | HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe | 120    |
| Db         | 400  | CATGGCCCCAAAGAGAGAAAGCGCTACCGAGCGTCCACGAACTGCACATTCGCAATTC   | 459    |
| Qy         | 121  | MetAlaSerLeuAlaThrHisPheSerArgLysAsnSerGlyIleIlePheSerSerVal | 140    |
| Db         | 460  | ATGGCTTCTTACGACACTCAGCTTACGACATCAGAACATGCGCATTAATCTTCAGCGATT | 519    |
| Qy         | 141  | GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer | 160    |
| Db         | 520  | GAGACCAACATTTGGAACCTCTTCATGTCTCATGACTGGGAATTTGGGCCCCCTATCA   | 579    |
| Qy         | 161  | GlyValTyrPhePheThrPheSerMetLeuTyrHisGluAspValGluGluVal       | 178    |
| Db         | 580  | GGTGTGTATTTCTTACCTTCACCTTCACATCATGATGATGACATGAGCAGTAGAGAGATG | 633    |
| RESULT 12  |  |  |        |
| LOCUS      | BB649178   | 703 bp.  | linear |
| DEFINITION | BB649178 RIKEN full-length enriched, 16 days embryo  | head   | mus    |
| ACCESSION  | musculus cDNA clone C13006D14 5', mRNA sequence.   |  |        |
| VERSION    | BB649178   |  |        |
| KEYWORDS   | BB649178.1 GI:16483433   |  |        |
| SOURCE     | EST.   |  |        |
| ORGANISM   | house mouse.   |  |        |
| REFERENCE  | Mus musculus   |  |        |
| AUTHORS    | Eukaryotes: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sclurognathi: Muridae: Murinae; Mus. 1 (bases 1 to 703)   |  |        |
| TITLE      | Atakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koyama,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,O., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.  |  |        |
| JOURNAL    | RIKEN Mouse ESTs (Atakawa,T., et al. 2001)   |  |        |
| COMMENT    | Unpublished (2001)<br>Contact: Yoshinide Hayashizaki<br>Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute<br>The Institute of Physical and Chemical Research (RIKEN)<br>1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan<br>Tel: 81-45-503-9222<br>Fax: 81-45-503-9216<br>Email: genome-res@gs.c.riken.go.jp,<br>URL: http://genome.gsc.riken.go.jp/<br>Carninci,P., Shibata,Y., Hayata,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.<br>Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)<br>waghi,K., Fujiyake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsuhiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.<br>RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)<br>Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.<br>Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)<br>Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamahata,I., Mizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.<br>Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)<br>Please visit our web site (http://genome.gsc.riken.go.jp) for further details. |  |        |

| FEATURES                                   | e mouse  |
|--|--|
| SOURCE                                     | tissues: Location/Qualifiers   |
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|  | /note="Site_1: Salt; Site_2: BamHI: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]<br>GAGGAGAAGAGATCCACAGACCTCTTTTTTTTTTTTNN 3'}. cDNA was prepared by using triethanol thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5']<br>GAGGAGAAGATCTCGAGTAATTAAATTAATCCCCCCCCCCC 3'}. cDNA was cloned into the XhoI and BamH sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLX I" |
| BASE COUNT                                 | 177 a 183 c 197 g 144 t 2 others   |
| ORIGIN                                     |  |
| Alignment Scores:                          |  |
| Pred. No.:                                 | 1.96e-81 Length: 703   |
| Score:                                     | 934.00 Matches: 171  |
| Percent Similarity:                        | 88.50% Conservative: 6   |
| Best Local Similarity:                     | 85.50% Mismatches: 22  |
| Query Match:                               | 68.32% Indels: 1   |
|  | Gaps: 0  |
| US-10-036-041-2 (1-246) x BB649178 (1-703) |  |
| OY   | 1 MetLeuTPRvGlnLeuLleTyrrTpGlInLeuAlaLeuPheLeuProPhcys 20<br>              ::  |
| Dd   | 96 ATGCTCGGGAGGCACGCGCATCTGGTGCGCACCTCGCTTCCTTGTCTCCCAATTTTGC 155  |
| OY   | 21 LeucySGlInAsPGluTYMeTClusePrGlnTrhgLygLYLeuProPaSPcySer 40<br>  |
| Dd   | 156 CTGTCTCAAGATGAATACATGAGGTCTCCACAAGCTGAGAGACTGCCCCCGACATCGACG 215   |
| OY   | 41 LysCySCySHISGLYASPTyrSerPheaTrgLYTrGnGLYProProGLYProProGLY 60<br>   |
| Dd   | 216 AAGTGTTCATGCGAGATTATGAGATTGTGTGTTCACAAAGGGCCCCCTCGACCTCCAGGT 275   |
| OY   | 61 ProProGLYLIEPRGLYASNHisGLYSnSnGLYASNsnGLYAlaThrGlyHISGLU 80<br>   |
| Dd   | 276 CCTCTGGGATTCCAGGAACCATGGAACAATGGAACATGGAACATGAGCATGCGCATGAA 335  |
| OY   | 81 GlyAlaLYSLyGLyGLyGLyGLYASPLySLySpleuGLYProTrgGLYLaArgLYSLN 100<br>  |
| Dd   | 336 GGGGCCAAGGTGAAGAAAGAGAACAAAGCGCACCTAGGCCCTCGAGGGAACGGGGGCGAG 395   |
| OY   | 101 HISGLYPROLYSGLYGLYSLyTYrProGLYIEPRProGLYULenGlnLEAlaPhe 120<br>  |
| Dd   | 396 CATGGCCCCCAAAGGAGACAAAGCGTACCAGGGGTGCCACCGAAGCTGCACATTCATTC 455  |
| OY   | 121 MetaIsERLeuAlaThrHisPheSerANGLINsnSERGLYLIEllePheSerSerVal 140<br>   |
| Dd   | 456 ATGGCTTCTTAGCAACATCTCACTTGCAGCAATCAGAAACAGGGCATTTATCTTCAGCAGTGT 515  |
| OY   | 141 GlutrasnILlegLYAsnPhePaSYALMetThrgLYArghneGLYAlaProVALser 160<br>  |
| Dd   | 516 GAGACCAACATTGGAAACTTCTTCGATCTCTGACTGGAGATTTGGGGCCCCCGTATCA 575   |



IMAGE:1920870 5', mRNA sequence.  
 A1316916  
 VERSION A1316916.1 GI:4032183  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 571)  
 REFERENCE  
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Giesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Treising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
 TITLE The WashU-HMI Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.wustl.edu  
 This clone is available royalty-free through LNL: contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
 MGI:977162  
 Seq primer: custom primer used  
 High quality sequence stop: 502.  
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 /sex="female"  
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 /lab\_host="DH10B"  
 /note="Organ: kidney; Vector: pME18S-FL3; Site\_1: DraIII (CACCTGTG); Site\_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer  
 [ATGCGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor (TGTGGCTACTGG), digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACCTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' and primer CTTCCTCTTAAAGCTGCG and 3' and primer CGACCTGACGCTCGACACA."  
 BASE COUNT 143 a 154 c 156 g 118 t  
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 Query Match: 60.02% Indels: 39  
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 QY 21 LeuGlySlnAspGluTyrMetGluSerProGlnThrGlyLeuProProAspCysSer 40  
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 Db 479 -----TTCAGCATGATGAGCATGAGCATGAGCATGAGCATGATGTGTG 520  
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 ACCESSION BG400260  
 VERSION BG400260.1 GI:13293708  
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 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 828)  
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: e9apbs-f@mail.nih.gov  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
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and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH/MGC Library."

BASE COUNT      233 a    182 c    190 g    223 t

ORIGIN

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| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
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US-10-036-041-2 (1-246) x BG400260 (1-828)

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OY 118 IleAlaPheMetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePhe 137
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DB 63  ATTGATTCATGCGCTCTCTGGCAACCCACTTCAGCAATCAGAAACAGTGGATATCTTC 122

OY 138 SerSerValGluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAla 157
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DB 123 AGCAGTGTGAGACCAACATTCGAAACTTCTTGATGTCATGACTGTGATTTGGGGCC 182

OY 158 ProValSerGlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGln 177
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DB 183 CCAGTATCAGGGTGTATTTCTTCACCTTCACATGATGATGATGATGATGATGATGATG 242

OY 178 ValTyrValTyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMet 197
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DB 303 AAGGCAATATCATGATACATCCAGCAATCATGCTGTGAGCTAGCCAAAGGGATGAG 362

OY 218 ValTyrPheValMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPhe 237
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DB 423 GCAGGATTCCTGCTCTTGAACCTAAG 449
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Search completed: January 15, 2003, 21:20:27  
Job time : 2243 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 15, 2003, 19:45:56 (Search time 97 Seconds

(without alignments)  
1130.759 Million cell updates/sec

Title: US-10-036-041-2

Perfect score: 1367

Sequence: 1 MWMRLIYWLALFLPFC.....LHGDRHSTFAGFLPETK 246

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 393868 seqs, 222934149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blcosum62  
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 4          | 849   | 62.1        | 1608   | 10 | US-09-822-849A-359 |

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| 13 | 293   | 21.4 | 1152 | 10 | US-09-776-976-1    | Sequence 1, Appl1  |
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| 25 | 290.5 | 21.3 | 3089 | 9  | US-09-997-653-46   | Sequence 46, Appl1 |
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#### ALIGNMENTS

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Sequence 1, Application US/10036041  
Publication No. US20020192751A1  
GENERAL INFORMATION:  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3030R1C8  
CURRENT APPLICATION NUMBER: US/10/036.041  
PRIOR FILING DATE: 2001-12-26  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/112514  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/113300  
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PRIOR FILING DATE: 1998-12-23



PRIOR APPLICATION NUMBER: 60/113605  
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PRIOR FILING DATE: 1999-05-14  
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PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30720  
PRIOR FILING DATE: 1999-12-22  
PRIOR APPLICATION NUMBER: PCT/US00/05601

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PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/17800  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: PCT/US01/19692  
PRIOR FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: PCT/US01/21066  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 80  
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LENGTH: 1712  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-036-041-1  
Alignment Scores:  
Pred. No.: 2,46e-117 Length: 1712  
Score: 1367.00 Matches: 246  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
US-10-036-041-2 (1-246) x US-10-036-041-1 (1-1712)  
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DB 77 ATCTTTGGAGCCAGCCATCATTTGGCAACTGCTGCTTTGTTTCCCTCTTTTGC 136  
QY 21 LeuCyGlnAspGlnIuYrMetGluSerProGlnThGlyGlyLeuProProAspCysSer 40  
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DB 197 AAGTGTTCATGAGACTACCTTTGAGGCTTACCAAGCCCTTGGGCCACCGGCC 256  
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DB 437 ATGGCTTCTCTGCAACCCACTTCACCAATCAGAAACAGTGGATTATCTTCACACAGTGT 496  
QY 141 GluThrAsnIleGlyAsnPhePheAspValMetThGlyArgPheGlyAlaProValSer 160  
DB 497 GAGACCAACATTTGGAACATCTTTGATGTCATACACGTGATGATTGGGGCCCAATATCA 556





PRIOR APPLICATION NUMBER: 09/380142  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/644848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 09/747259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 09/816744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: 09/854208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/854280  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/874503  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: 09/869599  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: 09/908, 827  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: PCT/US99/10733  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: PCT/US99/28551  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30720  
PRIOR FILING DATE: 1999-12-22  
PRIOR APPLICATION NUMBER: PCT/US00/05601  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: PCT/US00/14042  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: PCT/US00/23522  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/17800  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: PCT/US01/19692  
PRIOR FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: PCT/US01/21066  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 80  
SEQ ID NO 1  
LENGTH: 1712  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-036-342-1

Alignment Scores:  
Pred. No.: 2,466-117 Length: 1712  
Score: 1367.00 Matches: 246  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-10-036-041-2 (1-246) x US-10-036-342-1 (1-1712)

OY 1 MetLeuTrpArgGlnLeuIleTyrrTgInLeuLeuAlaLeuPheLeuPropheCys 20  
|||||  
DB 77 ATGCTTTGGAGGAGCTCATCTATTGGCAACTGCTTGTGTTTCTCCCTTTTGC 136  
leuCyGlnAspGlnLeuIleTyrrMetGlnSerProGlnThrGlyGlyLeuProAspCysSer 40  
|||||

DB 137 CTGTGTCAAGATGAATACATGAGTCTCCAAACCGAGAGACTACCCCACTGCAC 196  
OY 41 LysCyScySHISGLYAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60  
|||||  
DB 197 AAGGTGTTCATGGAGCTACAGCTTTCAGAGCTTACCAAGGCCCTTGGGCCACCGGGC 256  
OY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80  
|||||  
DB 257 CCTCTGTCATTCAGGAACCATGGAACATGGAACATGGAACATGGAACATGGAACATGGA 316  
OY 81 GlyAlaLysGlyGlyLysGlyLysAspLysGlyLysPleuGlyProArgGlyGluArgGlyGln 100  
|||||  
DB 317 GGAGCCAAAGGTGAGAAAGGCGACAAAGGTGACCTGGGGCTCGAGGGGCGGGGGCG 376  
OY 101 HisGlyProLysGlyGlyLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120  
|||||  
DB 377 CATGGCCCAAG 436  
OY 121 MetaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140  
|||||  
DB 437 ATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGACTGTT 496  
OY 141 GluTrpAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160  
|||||  
DB 497 GAGACCAACATGGAACCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 556  
OY 161 GlyValIyrPhePheThrPheSerMetLysHisGlyAspValGluGluValIyrVal 180  
|||||  
DB 557 GGTGTGTATTTCTTCACTTCAGCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 616  
OY 181 TyLeuMetHisAsnGlyAsnThrValPheSerMetLysSerTyrrSerTyrrGluMetLysGlyLys 200  
|||||  
DB 617 TACCTTATGCAATGCGCACACAGCTTCACGATTCATACGATTAATGAAGGCCAA 676  
OY 201 SerAspTrpSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValIyrPleu 220  
|||||  
DB 677 TCAGATACATCCAGCAATCATGCTGCTGAGAGCTGAGCAAGGGGATGAGGCTTGGCTG 736  
OY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240  
|||||  
DB 737 GCAATGGGCAATGGCGCTCTCCATGGGGACACCAACGCTTCACACCTTTCAGAGATT 796  
OY 241 LeuLeuPheGluThrLys 246  
|||||  
DB 797 CTGCTCTTTGAACCTAAG 814

RESULT 4  
US-09-822-849A-359  
Sequence 359, Application US/09822849A  
Patent No. US20020045170A1  
GENERAL INFORMATION:  
APPLICANT: Wong, Gordon G.  
APPLICANT: Clark, Hilary  
APPLICANT: Fechtel, Kim  
APPLICANT: Agostino, Michael J.  
APPLICANT: Howes, Steven H.  
APPLICANT: Resnick, Richard J.  
APPLICANT: Gulukota, Kamalakara  
APPLICANT: Graham, James R.  
APPLICANT: Genetics Institute, Inc.  
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
FILE REFERENCE: GIN 6403  
CURRENT APPLICATION NUMBER: US/09/822,849A  
PRIOR FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/195,582  
NUMBER OF SEQ ID NOS: 598  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 359  
LENGTH: 1608  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-822-849A-359

## Alignment Scores:

|                        |          |               |      |
|------------------------|----------|---------------|------|
| Pred. No.:             | 1,39e-69 | Length:       | 1608 |
| Score:                 | 849.00   | Matches:      | 159  |
| Percent Similarity:    | 100.00%  | Conservative: | 0    |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0    |
| Query Match:           | 62.11%   | Indels:       | 0    |
| DB:                    | 10       | Gaps:         | 0    |

US-10-036-041-2 (1-246) x US-09-822-849A-359 (1-1608)

```
QY 88 ASPPLSGLYASPLEUGLYPROARGLYGLUARGLYGLNHISGLYPROLYSGLYULYS 107
    |||
Db 2 GACAAAGTACCTGGGCGCTCGAGGGAGCGGGGCGCATGCGCCCAAGAGAGAG 61

QY 108 GLYTYRPROGLYLEUPROPGIULUENGLIILEPHESESERVALGUTHRASNIIEGLYASNPH 127
    |||
Db 62 GGTACCCGGGGATTCACAGAACTTCAGATTGCAATCTGCTTCGGCAACCCAC 121

QY 128 PHESEASNGIANSERGLYLEILEPHESESERVALGUTHRASNIIEGLYASNPH 147
    |||
Db 122 TTCAGCAATCAGAACAGTGGATTCCTTCAGCAGCTTCAGAACATTCGAAACTTC 161

QY 148 PHEASPVALMETHRGLYARGPHEGLYALAPROVALSERGLYVALTYRPHETHRPHE 167
    |||
Db 182 TTTCATGTCATGACGTGATGATTGGGGCCCGACGATACAGCTGTATTCTTCACCTTC 241

QY 168 SERMETELYSIHISGLUASPVALIGLUVALTYRVALTYRLEUMETHIASNGIYASN 187
    |||
Db 242 AGCATATGACATGATGAGGATGTTGAGGAGTATGCTTATGCAATGGCAAC 301

QY 188 THVALPHESEMETYRSETYRGLUMETLYSGLYSESERAPTHRESERASNHS 207
    |||
Db 302 ACGAGTTTCAGCATGTACAGCTTGAANTGAAGGCCAAATACATTCACCAATCAT 361

QY 208 ALAVALLEULYSLEUALAYSGLYASPGIUALTYRPLEUARGMETGLYASNGIYALA 227
    |||
Db 362 GCGTCTCTAAGCTACCAAGGGGATGAGGTTGGCTCGCAATGGCAATGGCGCTCTC 421

QY 228 HIASGLYASNHISGLNARPHESERTHRPHEALAGLYPHELEUMETHRGLYULYS 246
    |||
Db 422 CATGGGACCAACCAAGCTTCTCCACCTTGGCAGATTCCTCTTTGAACCTAAG 478
```

## RESULT 5

US-09-728-952-85

Sequence 85, Application US/09728952

Patent No. US20020111302A1

## GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Zhou, Ping

APPLICANT: Goodrich, Ryle

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Wang, Jian-Rui

APPLICANT: Yamazaki, Vicki

APPLICANT: Ujwal, Manusha L.

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. US20020111302A1el Nucleic Acids and

FILE REFERENCE: 799

CURRENT APPLICATION NUMBER: US/09/728, 952

NUMBER OF SEQ ID NOS: 101

SOFTWARE: PC-FL-Genes Version 2.0

SEQ ID NO 85

LENGTH: 1297

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (80)..(949)

US-09-728-952-85

## Alignment Scores:

|                        |          |               |      |
|------------------------|----------|---------------|------|
| Pred. No.:             | 1,94e-20 | Length:       | 1297 |
| Score:                 | 315.00   | Matches:      | 86   |
| Percent Similarity:    | 41.26%   | Conservative: | 32   |
| Best Local Similarity: | 30.07%   | Mismatches:   | 96   |
| Query Match:           | 23.04%   | Indels:       | 72   |
| DB:                    | 10       | Gaps:         | 9    |

US-10-036-041-2 (1-246) x US-09-728-952-85 (1-1297)

```
QY 14 LEUPHEPHELEUPROPHCYSLUCYSLNAPGLUTYRMEGLUSERPROGINTHRGLY 33
    |||
Db 92 CTCTATGTTACAACTTTTGCATTGTGCCAGTGCACAAACCCGGGTAACTGAGAA 151

QY 34 GLYLEUPROPHASPCYSSELYSCYSCYSHISGLYSPHYSERPHEARGLYTYGLN 53
    |||
Db 152 GGAGAGACTACTCCGCCAGATATATCTCC-----ACCATTCCTCGCTTCCT 199

QY 54 GLYPROGLYPROPGIULUENGLIILEPHESESERVALGUTHRASNIIEGLYASN 73
    |||
Db 200 GGAACCTCCAGGGCCCTCGAGCAATGTTCCCTGGGCCCATGATGCTCATCGCTTC 259

QY 74 ASNGIYALATHRGLYHISGLUVALYALYSGLYULYSGLYASP----- 88
    |||
Db 260 CCAAGAGAGATGTTAGACAGCGCAGAAAGAGAGAAAGTGAAGAAGCACTGCAGT 319

QY 88 ----- 88
    |||
Db 320 TTGAGAGTAAGACTGACCGCTAGCTTCGCCGTGAGAAAGGAGCAAGAGACT 379

QY 89 -----LYSGLYASPLEUGLYPROARGLYGLUARGLYGLNHISGLYPRO----- 103
    |||
Db 380 GCGAAGAAAGACCCATAGGACAGAGGAGAGAAAGAAAGTGAAGTCCAAATGGTCT 439

QY 104 -----LYSGLYGLULYSGLYTYRPROGLYLEUPRO----- 114
    |||
Db 440 CTTGACCAAAAGGAGACAGAGAGCAAGACAGGACCGGCGCTGAGATTTCGAGA 499

QY 115 -----GLULEUGLIILEAPHEMETALASERLEUALATHRHPHESEASN 130
    |||
Db 500 TGTGGAAGACTCGTCAATACCGCTTTCTGTTGGCATCACACACCTACCCAGAA 559

QY 131 GLNANSERCGLYLEILEPHESESERVALGUTHRASNIIEGLYASNPHASPVAL 150
    |||
Db 560 GAAAGACTACTATATATTTAACAGGCTCTTCACAGGAGGAGCACTACACCT 619

QY 151 METHRGLYARGPHEGLYALAPROVALSERGLYVALTYRPHETHRPHESEMETCT 170
    |||
Db 620 GCCACAGAGGAGTTCATCTGCTTCACAGGATCATTTCTTATGATATACACA 679

QY 171 -----LYSHISGLUASPVALIGLUVALTYRVALTYRLEUMETHIASNGIYASN 187
    |||
Db 680 TTGCTAATAGCAT-----CTGGCAATCGAGCTGTACAAATGGG--- 721

QY 188 THVALPHESEMETYRSETYRGLUMETLYS-----GLYLYSER 201
    |||
Db 722 -----CAATACCGGATTAAGACTTCACGCCCAACACAGAAACCAT 763

QY 202 ASPTHSESERASNHSIALAVALLEULYSLEUALAYSGLYASPGIUALTYRPLEUARG 221
    |||
Db 764 GATGTGCTTCGGGGTCCACAGTCAATCTATCTGAGCACAAGATGAAGTCTGGCTGAG 823

QY 222 MET-----GLYASNGIYALALEUHHISGLYASPHISGLNARGPHESETHRPH 237
    |||
Db 824 ATTTTCTTCACAGACCAAGATGCTTCTTCAGACCCAGGTGGGAGACACCTATTTC 883

QY 238 ALAGLYPHELEUPHE 243
    |||
Db 884 TCCGGGTTCTTTATAC 901
```

## RESULT 6

US-09-776-976-3

Sequence 3, Application US/09776976  
Patent No. US20020037849A1  
GENERAL INFORMATION:  
APPLICANT: Eruebis, Joachim  
APPLICANT: Erickson, Mary Ruth  
APPLICANT: Yen, Frances  
APPLICANT: Bihain, Bernard  
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass  
FILE REFERENCE: 76 USA REG  
CURRENT APPLICATION NUMBER: US/09/776,976  
CURRENT FILING DATE: 2001-02-05  
PRIOR APPLICATION NUMBER: US 09/758,055  
PRIOR FILING DATE: 2001-01-10  
PRIOR APPLICATION NUMBER: US 60/176,228  
PRIOR FILING DATE: 2000-01-14  
PRIOR APPLICATION NUMBER: US 60/198,087  
PRIOR FILING DATE: 2000-04-13  
PRIOR APPLICATION NUMBER: US 60/299,881  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent.pm  
SEQ ID NO 3  
LENGTH: 1276  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-776-976-3

Alignment Scores:  
Pred. No.: 5.69e-19 Length: 1276  
Score: 299.00 Matches: 82  
Percent Similarity: 47.10% Conservative: 40  
Best Local Similarity: 31.66% Mismatches: 103  
Query Match: 21.87% Indels: 34  
DB: 10 Gaps: 9

US-10-036-041-2 (1-246) x US-09-776-976-3 (1-1276)

OY 4 ATGAGlnleuileTyrTrpInleuAlaLeuPhePheProPheCysLeuGln 23  
DB 43 AGAGAGCTACTGTGCAAGCTCTCTCTCTTAACTCTGCCC---AGTCATGCCGA 99  
OY 24 ASPgluTyrMetGluSerProGlnThrGlyGly-----LeuProPaspCysSerLys 41  
DB 100 GATGAGCTTACTACACTAGAGAGCTAGCTCTGCTTGTGCTCCACCAAGGAACT 159  
OY 42 CysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGlyPro 61  
DB 160 TGTGCA-----GGTTGGATGCA-----GGCATC 183  
OY 62 ProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGly 81  
DB 184 CCAAGGACATCTGGGACATGACACCAAGCCGCTGATGAGAGATGCACTCTCTGTA 243  
OY 82 ATATyGlnGlyIleGlyAspLysPryGlyAspLysPryGlyProArgGlyGlnArg----- 98  
DB 244 GAGAAAGGAGAAAGAGATGACAGCTCTCTGTCCTTAAGGTCAGACAGAGATGTT 303  
OY 99 GlyGlnHisGlyProGlyGlyAspLysGlyTyrProGlyIleProProGly----- 115  
DB 304 GGAATGACAGAGCTGAGGACGACGCGCTTCCCGGACCCCTGGAGAAAGAGAG 363  
OY 116 -----LeuGlnIleAlaPheMetAlaSerLeuAlaThrHisPhe 128  
DB 364 CCTGGAAGACCGCTTATATGATCGCTCAGCGTTCAGTGGGGCTGGAGACCGCGTC 423  
OY 129 SerAspGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhePhe 148  
DB 424 ACCTGTTCCCAATGTACCACTTCGCTTACTAGATCTTCTACACCAAGAAATCTTAT 483  
OY 149 AspValMetThrGlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPheSer 168  
DB 484 GACGCGAGACTGTGCAAGTTCATGTCACAACTCCGCGACTCTACTACTTCTTACAC 543

OY 169 MetMetLysHisGlyAspValGluGlyValTyrValTyrLeuMetHisAsnGlyAsnThr 188  
DB 544 ATCAGCGGTAC-----ATGAAGATGTGAAGGTGAGGCTCTTCAAGAGCAAGGCC 597  
OY 189 ValPheSerMetLysSerTyrGlnMetLysGlyLysSerAspThrSerSerAsnHisAla 208  
DB 598 GTTCTCTTCACCTACGACCAAGATGACAGAAAGAAATGTGGACAGCCCTTGCTGTG 657  
OY 209 ValLeuLysLeuAlaLysGlyAspGlyValTyrPheArgMet---GlyAsnGly----- 225  
DB 658 CTCCTCATCTGAGGTGGAGACCAAGTGTGGCTCAGGTATGGGATGGGAGCCAC 717  
OY 226 ---AlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuPhe 243  
DB 718 ATGCACTGTATGACAGATACGTACAGCAAGCACTGACTTACTGCTTCTCTAC 774

RESULT 7

US-09-758-055-3  
Sequence 3, Application US/09758055  
Patent No. US20020058617A1  
GENERAL INFORMATION:

APPLICANT: Eruebis, Joachim  
APPLICANT: Erickson, Mary Ruth  
APPLICANT: Yen, Frances  
APPLICANT: Bihain, Bernard  
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass  
FILE REFERENCE: 76 USA REG  
CURRENT APPLICATION NUMBER: US/09/758,055  
CURRENT FILING DATE: 2001-01-10  
PRIOR APPLICATION NUMBER: US 60/176,228  
PRIOR FILING DATE: 2000-01-14  
PRIOR APPLICATION NUMBER: US 60/198,087  
PRIOR FILING DATE: 2000-04-13  
PRIOR APPLICATION NUMBER: US 60/299,881  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent.pm  
SEQ ID NO 3  
LENGTH: 1276  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-758-055-3

Alignment Scores:

Pred. No.: 5.69e-19 Length: 1276  
Score: 299.00 Matches: 82  
Percent Similarity: 47.10% Conservative: 40  
Best Local Similarity: 31.66% Mismatches: 103  
Query Match: 21.87% Indels: 34  
DB: 10 Gaps: 9

US-10-036-041-2 (1-246) x US-09-758-055-3 (1-1276)

OY 4 ATGAGlnleuileTyrTrpInleuAlaLeuPhePheProPheCysLeuGln 23  
DB 43 AGAGAGCTACTGTGCAAGCTCTCTCTCTTAACTCTGCCC---AGTCATGCCGA 99  
OY 24 ASPgluTyrMetGluSerProGlnThrGlyGly-----LeuProPaspCysSerLys 41  
DB 100 GATGAGCTTACTACACTAGAGAGCTAGCTCTGCTTGTGCTCCACCAAGGAACT 159  
OY 42 CysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGlyPro 61  
DB 160 TGTGCA-----GGTTGGATGCA-----GGCATC 183  
OY 62 ProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGly 81  
DB 184 CCAAGGACATCTGGGACATGACACCAAGCCGCTGATGAGAGATGCACTCTCTGTA 243  
OY 82 ATATyGlnGlyIleGlyAspLysPryGlyAspLysPryGlyProArgGlyGlnArg----- 98  
DB 244 GAGAAAGGAGAAAGAGATGACAGCTCTCTGTCCTTAAGGTCAGACAGAGATGTT 303





NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent.pm  
SEQ ID NO 5  
LENGTH: 4517  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-776-976-5

Alignment Scores:  
Pred. No.: 9,35e-18 Length: 4517  
Score: 293.50 Matches: 83  
Percent Similarity: 47.45% Conservative: 38  
Best Local Similarity: 32.55% Mismatches: 96  
Query Match: 21.47% Indels: 39  
DB: 10 Gaps: 11

US-10-036-041-2 (1-246) x US-09-776-976-5 (1-4517)

```
OY 9 TTPGInLeuAlaLeuPhePheLeuProPheCysLeuCysGlnAspGluTyrMetGlu 28
   |||:|||||
   |||:|||||
DB 37 TGGGAGCTG-----TTCTACTGCTATTAGCTGCGCCGGC---ATGACCAGG 81
   |||:|||||
OY 29 SerProGlnThGlyGlyLeuProProAspCysSerLysCysCysHisGlyAspTyrSer 48
   |||:|||||
DB 82 AACCACGACATCAAGGCG---CCGAGCTCTGCTCCCTCCGCCCAAGGGG----- 129
   |||:|||||
OY 49 PheArgGlyTyrGlnGlyProProGlyProProGlyProProGlyTyrLeProGlyAsnHis 68
   |||:|||||
DB 130 -----CTGCACAGCTTGATG---GCGGGCATCCCAAGGCGATCCG 167
   |||:|||||
OY 69 GLYAsnAsnGlyAsnAsnGlyAlaThrGlnHisGlnGlyAlaGlyGlyGlyAsp 88
   |||:|||||
DB 168 GGCCTAATATGGGGCCCGCCAGCGGTGATGCGAGATGGACCCCTGGTGAGAGGGTGA 227
   |||:|||||
OY 89 LysGlyAsp-----LeuGlyProArg-----GlyGluArgGlyGlnHisGly 102
   |||:|||||
DB 228 AAGAGAGATCCAGCTTATTGGTCTTAAGGAGACATCGGTGAACCGGACTACCCGG 287
   |||:|||||
OY 103 ProLysGlyGlyLysGlyTyrProGlyTyr-----ProProGlu--- 115
   |||:|||||
DB 288 GCTGAAGTCCCGCGAGCTTCCGGGAATCCAAAGCAGAAAGAGAACTGGAGAGAGT 347
   |||:|||||
OY 116 -----LeuGlnIleAlaPheMetAlaSerLeuAlaThrHisPheSerAsnGlnAsn 132
   |||:|||||
DB 348 GCCTATGATATACCGCTCACTAGCTGGATGGAGACTATGATCTATCCCAAC 407
   |||:|||||
OY 133 SerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhePheAspValMetThr 152
   |||:|||||
DB 408 ATGCCCATTCGCTTATACCAAGATCTTCAATCAATCAAGCAAAACCACTATATGCTCCACT 467
   |||:|||||
OY 153 GlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPheSerMetLysHis 172
   |||:|||||
DB 468 GGTAAATATCCACTGCAACATCTCCGGCTGTACTTCTGCTACACATCAAGTCTAT 527
   |||:|||||
OY 173 GluAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsnThrValPheSerMet 192
   |||:|||||
DB 528 -----ATGAAAGATGTGAAGGTCAAGCTCTCAAGAAAGACAAAGGCTATGCTTCCACC 581
   |||:|||||
OY 193 TyrSerTyrGluMetLysGlyLysSerAspThrSerSerAsnHisAlaValLeuLysLeu 212
   |||:|||||
DB 582 TATGATCACTACCAAGAAATATATGTGACCAAGCCCTCCGGCTGTGCTCTCTGCTCATG 641
   |||:|||||
OY 213 AlaLysGlyAspGluValTyrLeuArgMet---GlyAsnGly-----AlaLeuHis 228
   |||:|||||
DB 642 GAGGTGGCGGCAAGTATGCTGCTCCAGGTGTATGGGAAGAGAGAGGTATGAGACTATAT 701
   |||:|||||
OY 229 GlyArgHisGluArgPheSerThrPheAlaGlyPheLeuPhe 243
   |||:|||||
DB 702 GCTGATATGACAAATGACTCCACCTTCCAGAGCTTCTTCTCTAC 746
   |||:|||||
```

Patent No. US20020058617A1  
GENERAL INFORMATION:  
APPLICANT: Fruedlis, Joachim  
APPLICANT: Erickson, Mary Ruth  
APPLICANT: Yen, Frances  
APPLICANT: Bihain, Bernard  
TITLE OF INVENTION: ORG3 Globular Head and Uses Thereof for Decreasing Body Mass  
FILE REFERENCE: 76 US4 REG  
CURRENT APPLICATION NUMBER: US/09/758,055  
PRIORITY FILING DATE: 2001-01-10  
PRIORITY APPLICATION NUMBER: US 60/176,228  
PRIORITY FILING DATE: 2000-01-14  
PRIORITY APPLICATION NUMBER: US 60/198,087  
PRIORITY FILING DATE: 2000-04-13  
PRIORITY APPLICATION NUMBER: US 60/299,881  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent.pm  
SEQ ID NO 5  
LENGTH: 4517  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-758-055-5

Alignment Scores:  
Pred. No.: 9,35e-18 Length: 4517  
Score: 293.50 Matches: 83  
Percent Similarity: 47.45% Conservative: 38  
Best Local Similarity: 32.55% Mismatches: 96  
Query Match: 21.47% Indels: 39  
DB: 10 Gaps: 11

US-10-036-041-2 (1-246) x US-09-758-055-5 (1-4517)

```
OY 9 TTPGInLeuAlaLeuPhePheLeuProPheCysLeuCysGlnAspGluTyrMetGlu 28
   |||:|||||
   |||:|||||
DB 37 TGGGAGCTG-----TTCTACTGCTATTAGCTGCGCCGGC---ATGACCAGG 81
   |||:|||||
OY 29 SerProGlnThGlyGlyLeuProProAspCysSerLysCysCysHisGlyAspTyrSer 48
   |||:|||||
DB 82 AACCACGACATCAAGGCG---CCGAGCTCTGCTCCCTCCGCCCAAGGGG----- 129
   |||:|||||
OY 49 PheArgGlyTyrGlnGlyProProGlyProProGlyProProGlyTyrLeProGlyAsnHis 68
   |||:|||||
DB 130 -----CTGCACAGCTTGATG---GCGGGCATCCCAAGGCGATCCG 167
   |||:|||||
OY 69 GLYAsnAsnGlyAsnAsnGlyAlaThrGlnHisGlnGlyAlaGlyGlyGlyAsp 88
   |||:|||||
DB 168 GGCCTAATATGGGGCCCGCCAGCGGTGATGCGAGATGGACCCCTGGTGAGAGGGTGA 227
   |||:|||||
OY 89 LysGlyAsp-----LeuGlyProArg-----GlyGluArgGlyGlnHisGly 102
   |||:|||||
DB 228 AAGAGAGATCCAGCTTATTGGTCTTAAGGAGACATGCGTGAACCGGACTACCCGG 287
   |||:|||||
OY 103 ProLysGlyGlyLysGlyTyrProGlyTyr-----ProProGlu--- 115
   |||:|||||
DB 288 GCTGAAGTCCCGCGAGCTTCCGGGAATCCAAAGCAGAAAGAGAACTGGAGAGAGT 347
   |||:|||||
OY 116 -----LeuGlnIleAlaPheMetAlaSerLeuAlaThrHisPheSerAsnGlnAsn 132
   |||:|||||
DB 288 GCTGAAGTCCCGCGAGCTTCCGGGAATCCAAAGCAGAAAGAGAACTGGAGAGAGT 347
   |||:|||||
OY 133 SerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhePheAspValMetThr 152
   |||:|||||
DB 408 ATGCCCATTCGCTTATACCAAGATCTTCAATCAATCAAGCAAAACCACTATATGCTCCACT 467
   |||:|||||
OY 153 GlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPheSerMetLysHis 172
   |||:|||||
DB 468 GGTAAATATCCACTGCAACATCTCCGGCTGTACTTCTGCTACACATCAAGTCTAT 527
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OY 173 GluAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsnThrValPheSerMet 192
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DB 528 -----ATGAAAGATGTGAAGGTCAAGCTCTTCAAGAAAGACAAAGGCTATGCTTCCACC 581
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```



```

Db      82 AAACGACGACTAAGGCG---CCGAGTCTGCTCCCTCCCAAGGCGG-----129
Oy      49 PheArgGlyTYrGlnGlyProProGlyProProGlyProProGlyIleProGlyAsnHis 68
Db      130 -----CCTGCACAGTTGGATG-GCGGGCATCCACAGGATCCG 167
Oy      69 GlysAsnGlnGlyAsnGlnGlyAlaThrGlnHisGlnGlyAlaGlyGlnGlyAsp 88
Db      168 GGCATTAATGGGGCCCCAGGCGCGTGGATGGCAGATGGCACCCTGGGTGGAGAGGGTGAG 227
Oy      89 LysGlyAsp-----LeuGlyProArg-----GlyGluArgGlyGlnHisGly 102
Db      228 AAAGAGATCCAGGCTTATGTGCTTAAGGAGACATCGGTAACCGGATACCCGGC 287
Oy      103 ProLysGlyGlyGlyTYrProGlyIle-----ProGlu--- 115
Db      288 GCTGAAGTCCCGCAGGCTTCCGGGAATCCAGGCAAGGCAAGAACTGGAGAGGT 347
Oy      116 -----LeuGlnIleAlaPheMetAlaSerIleuAlaThrHisPheSerAsnGlnAsn 132
Db      348 GCGTATGTAATCCGCTACGATCACTGCTGGATTGAGACTTACGTTACTATCCCAAC 407
Oy      133 SerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPheAspValMetThr 152
Db      408 ATGCCCATTCCTTACACAGATCTTACAAATCAGCAAAACCACTATGATGGCTCCACT 467
Oy      153 GlyArgPheGlyAlaProValSerGlyValTYrPhePheThrPheSerMetGlyHis 172
Db      468 GGTAAATCCCTGCAACATTCCTGGGCTGTAATCTTGGCTTCCACATCAGTCTAT 527
Oy      173 GlnAspValGlnGluValTYrValTYrLeuMetHisAsnGlyAsnThrValPheSerMet 192
Db      528 -----ArgAAAGATGTGAAGTCAAGCTCAGCTTTCAGAAAGACAGCAAGCTTTCACC 581
Oy      193 TyrSerTYrGluMetLysGlyLysSerAspThrSerSerAsnHisAlaValLeuGlyLeu 212
Db      582 TATGATCAGTACAGGAATAATATGTGACCAAGGCTCGGCTGTGGCTCTGCACTCG 641
Oy      213 AlaLysGlyAspGluValTYrPheuArgMet---GlyAsnGly-----AlaLeuHis 228
Db      642 GAGGTGGCGGCAAGAGTGGCTGCAGGCTGTAATGGGAAAGAGAGCAATGAGCTATAT 701
Oy      229 GlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuPhe 243
Db      702 GCTGTAATGACATGACTCCACCTTCACAGGCTTCTTCTCTAC 746

RESULT 13
US-09-776-976-1
; Sequence 1, Application US/09776976
; Patent No. US20020037849A1
; GENERAL INFORMATION:
; APPLICANT: Friedbis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihaio, Bernard
; TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76.USA.REG
; CURRENT APPLICATION NUMBER: US/09/776,976
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/758,055
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/176,228
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/198,087
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/299,881
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 1152
; TYPE: DNA

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; ORGANISM: mus musculus
; US-09-776-976-1

Alignment Scores:
Pred. No.: 1,786-18 Length: 1152
Score: 293.00 Matches: 81
Percent Similarity: 46.54% Conservative: 40
Best Local Similarity: 31.15% Mismatches: 99
Query Match: 21.43% Indels: 40
Db: 10 Gaps: 10

US-10-036-041-2 (1-246) x US-09-776-976-1 (1-1152)
Oy      6 LeuIleTYrTrGlnLeuLeuAlaLeuPhePheLeuProPheCysLeuGlyAsnGln 25
Db      20 CTACTGTTCCAGACTCTCTCTGTTCTTAAATCTGCCC---AGTCATGCCGAGATGAC 76
Oy      26 TYrMetGluSerProGlnThrGlyGly-----LeuProAspCysSerLysCys 43
Db      77 GTTACTACAACTGAGAGAGCTACTCTCTGTTGGTCTTCCCTCCACCCCAAGGAACTTGCA 136
Oy      44 HisGlyAspTYrSerPheArgGlyTYrGlnGlyProProGlyProProGlyProProGly 63
Db      137 -----GTTGGATGCGCA-----GGC 151
Oy      64 IleProGlyAsnHisGlyAsnAsnGlyAsnGlnGlyAlaThrGlnHisGlnGlyAlaLys 83
Db      152 ATCCCGGACATTCCTGGCCACAAATGGCACACCGAGCGGTGATGGCAGAGATGGCACTCT 211
Oy      84 GlyGlyLysGlyAspLysGlyAsp-----LeuGlyProArgGlyGluArg----- 98
Db      212 GGAGAGAAAGAGAGAGAAAGAGATTCAGGCTTCTTGGTCTTAAGGTGAGACAGAGAT 271
Oy      99 ---GlyGlnHisGlyProLysGlyGlyTYrProGlyIleProProGlu----- 115
Db      272 GTTGGAAATGACAGAGACTGAGGCTCGGGGCTTCCCGGAACCTTCGACAGAAAGCA 331
Oy      116 -----LeuGlnIleAlaPheMetAlaSerIleuAlaThrHis 127
Db      332 GAGCTGGCAAAACCCCTTATGTCTGATCGCTCAGGCTTACAGTGGGCTGGAGACCCGC 391
Oy      128 PheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhe 147
Db      392 GTCACCTGTTCCCAATGATACCAATTCGCTTACTAAGATGTCTACAAACAAGAAATCAT 451
Oy      148 PheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTYrPhePheThrPhe 167
Db      452 TATGACAAACAGCACTGGCAAGTTCTACTGCAACATTCGCGGACTTACTACTCTCTTAC 511
Oy      168 SerMetMetLysHisGlnAspValGlnGluValTYrValTYrLeuMetHisAsnGlyAsn 187
Db      512 CACATCAGCGGTAC-----ArgAAAGATGTGAAGTGAAGCTTTCAGAAAGACAAAG 565
Oy      188 ThrValPheSerMetLysGlyGluMetLysGlyLysSerAspThrSerSerAsnHis 207
Db      566 GCCGTTCTTCACTACACAGCAAGTACAGAAATAATGTGACCAAGGCTCTGGCTGCT 625
Oy      208 AlaValLeuLysLeuAlaLysGlyAspGluValTYrPheuArgMet---GlyAsnGly--- 225
Db      626 GTGCTCTTCATCTGAGAGTGGGAGACCAAGTCTGCTCAGGCTGTAATGGGAGTGGGAG 685
Oy      226 -----AlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuPhe 243
Db      686 CACAAATGACTATGCAAGATACGTAACAGCACTATCACTTACTGCGTTCTTCTTCT 745

RESULT 14
US-09-758-055-1
; Sequence 1, Application US/09758055
; Patent No. US20020058617A1
; GENERAL INFORMATION:
; APPLICANT: Friedbis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances

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Oy 116 -----LeuGlnIleAlaPheMetAlaSerLeuAlaThrHis 127
Db 332 GAGCCTGGAGAAAGCCGCTTATGCTATGCTACGCTTCAGGCTTCAGTGGGGCTGGAGACCCGC 391
Oy 128 PheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhe 147
Db 392 GTCACTGTCCCAATGTAATGCCATTCGCTTACTAGATCTTACACACACAGAAATCAT 451
Oy 148 PheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPhe 167
Db 452 TATGACAAACAGCAGCTGGCAAGTTCTACTGCAACATTCGCGGACTCTACTACTCTCTTAC 511
Oy 168 SerMetMetLysHisGlnAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsn 187
Db 512 CACATCAGCGGTAC-----ATGAAAGATGTGAAGGTGAGGCTCTTCAAGAGACAAAG 565
Oy 188 ThrValPheSerMetLysSerTyrGluMetLysGlyLysSerAspThrSerSerAsnHis 207
Db 566 GCCGTTCTCTTACCTACCTACGACACAGTATCAGAAAGAAATGTGAGCAGGCTCTGCTCT 625
Oy 208 AlaValLeuLysLeuAlaLysGlyAspGluValTrpLeuArgMet--GlyAsnGly--- 225
Db 626 GTGCTCTCTCATCTGAGAGGTGGAGACCAAGCTGCTCCAGGTCTATGAGGATGGGAGAC 685
Oy 226 -----AlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPhe 243
Db 686 CACAATGAGACTCTATGACAGTAAAGCTCAAGACTTACATTACGTGCTTCTCTCTTC 745
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Search completed: January 15, 2003, 21:23:46  
Job time : 106 secs



23-MAR-1999: 99US-0125774.  
PR 23-MAR-1999: 99US-0125778.  
PR 24-MAR-1999: 99US-0125826.  
PR 31-MAR-1999: 99US-0127035.  
PR 05-APR-1999: 99US-012706.  
PR 21-APR-1999: 99US-0130359.  
PR 27-APR-1999: 99US-0131270.  
PR 27-APR-1999: 99US-0131272.  
PR 27-APR-1999: 99US-0131291.  
PR 04-MAY-1999: 99US-0132371.  
PR 04-MAY-1999: 99US-0132379.  
PR 04-MAY-1999: 99US-0132383.  
PR 25-MAY-1999: 99US-0135250.  
PR 08-JUN-1999: 99US-0138166.  
PR 20-JUL-1999: 99US-0144791.  
PR 03-AUG-1999: 99US-0146970.  
PR 09-DEC-1999: 99US-0170262.  
XX  
PA (GETH ) GENENTECH INC.  
PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;  
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;  
XX  
DR WPI: 2000-628263/60.  
DR P-PSDB: AAB18909.  
XX  
PT Novel secreted and transmembrane polypeptides useful for diagnosing  
PT tumour in a mammal, for identifying agonists and antagonists of the  
PT polypeptide and for therapeutic use  
XX  
PS Claim 2: Fig 1; 222pp; English.  
XX  
CC The present sequence encodes a secreted or transmembrane polypeptide.  
CC The specification describes polypeptides designated PRO1484, PRO434,  
CC PRO1122, PRO1889, PRO1890, PRO1785, PRO4353, PRO4405,  
CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5337, PRO4425, PRO5990,  
CC PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is  
CC useful for diagnosing tumour in a mammal. The polypeptides, their  
CC agonists and antagonists are useful treating a condition associated with  
CC expression or activity of the polypeptide. Conditions treated include  
CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are  
CC capable of inducing proliferation of mammalian kidney mesangial cells  
CC and are therefore useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger's disease or other  
CC nephropathies associated with Schönlein-Henoch purpura, celiac disease,  
CC dermatitis herpetiformis or Crohn's disease. The nucleic acids may be used  
CC to generate transgenic animals for use in development and screening of  
CC therapeutically useful reagents and also for chromosome identification  
CC and tissue typing.  
XX  
SQ Sequence 1712 BP; 491 A; 358 C; 388 G; 475 T; 0 other:  
Query Match 99.9%; Score 1710.4; DB 21; Length 1712;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1711; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 GGCATCTGCCCCGAGAGACACACGCTCTGAGAGCTGCTGCTTCTTCAGGAGACTCTGA 60  
DB 1 GGCATCTGCCCCGAGAGACACACGCTCTGAGAGCTGCTGCTTCTTCAGGAGACTCTGA 60  
OY 61 GGCCTGTGTGAATCAATGCTTTGGAGGACACTATCTATTGGCACTGCTGGCTTTGTT 120  
DB 61 GGCCTGTGTGAATCAATGCTTTGGAGGACACTATCTATTGGCACTGCTGGCTTTGTT 120  
OY 121 TTTCCTCCCTTTTGGCTGTGTCAAGATGAATACATGAGAGTCTCCACAAACCGAGAGACT 180  
DB 121 TTTCCTCCCTTTTGGCTGTGTCAAGATGAATACATGAGAGTCTCCACAAACCGAGAGACT 180  
OY 181 ACCCCCAACAGCTAGTAACTGTGTGATGAGAGACTACAGCTTTTGGAGGCTTCCAAAGGCC 240  
DB 181 ACCCCCAACAGCTAGTAACTGTGTGATGAGAGACTACAGCTTTTGGAGGCTTCCAAAGGCC 240  
OY 241 CCTGGGCGACCGGGCCCTCTGGCATTCAGGAACCATGGAACATGCGACAAATG 300

|||||  
DB 241 CCTGGGCGACCGGGCCCTCTGGCATTCAGGAACCATGGAACATGCGACAAATG 300  
OY 301 AGCCACTGTGTATAGAGAGCCAAAGGTGAGAGGGGACAAAGGTGACCTGGGCGCTCG 360  
DB 301 AGCCACTGTGTATAGAGAGCCAAAGGTGAGAGGGGACAAAGGTGACCTGGGCGCTCG 360  
OY 361 AGGGGACCGGGGCGAGCATGGCCCCCAAGGAGAGAGGGGCTACCCGGGGATTCACACGA 420  
DB 361 AGGGGACCGGGGCGAGCATGGCCCCCAAGGAGAGAGGGGCTACCCGGGGATTCACACGA 420  
OY 421 ACTTCAGATTTCATTCATGAGCTTCTGTGCAACCCACTTCAGCATTCAGAACTAGGAGT 480  
DB 421 ACTTCAGATTTCATTCATGAGCTTCTGTGCAACCCACTTCAGCATTCAGAACTAGGAGT 480  
OY 481 TATCTTCAGCAGTGTGAGACCAACATTTGAACCTCTTGTGATGTGATGACTGTAGATT 540  
DB 481 TATCTTCAGCAGTGTGAGACCAACATTTGAACCTCTTGTGATGTGATGACTGTAGATT 540  
OY 541 TGGGGCCCCAGTATCAGGTGTGTATTTCTTACCTTCAGCATGATGAGCATGAGATGT 600  
DB 541 TGGGGCCCCAGTATCAGGTGTGTATTTCTTACCTTCAGCATGATGAGCATGAGATGT 600  
OY 601 TGAGGAGTGTATGTATGATCTTATGCAACATGGGACAGAGCTTCAGCATGTACAGCTA 660  
DB 601 TGAGGAGTGTATGTATGATCTTATGCAACATGGGACAGAGCTTCAGCATGTACAGCTA 660  
OY 661 TGAATGAGGGCAATTCAGATACATCCAGCAATCATCTGTGTGAAGTACCAAGG 720  
DB 661 TGAATGAGGGCAATTCAGATACATCCAGCAATCATCTGTGTGAAGTACCAAGG 720  
OY 721 GGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTTCATGGGACCAACACGCTTCTC 780  
DB 721 GGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTTCATGGGACCAACACGCTTCTC 780  
OY 781 CACCTTTGACAGATTCCTGCTCTTTGAACTAGTAATATATGCTAGATAGCTCCAC 840  
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OY 841 TTTGGGGAAGACTGTGACCTGAGCTGATTTGTAGCATCTGAGGAACATTAAGTTGAG 900  
DB 841 TTTGGGGAAGACTGTGACCTGAGCTGATTTGTAGCATCTGAGGAACATTAAGTTGAG 900  
OY 901 GTTTTACATCTCTGTATTCAAAAAATTTTGGTTCATATGTTGTTGACGCTACAGTACA 960  
DB 901 GTTTTACATCTCTGTATTCAAAAAATTTTGGTTCATATGTTGTTGACGCTACAGTACA 960  
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DB 1081 TCTCTCTGAGGAGGTTGGAATATTTTCTTATCAGAGAGATTCATTTGGAAGAATT 1140  
OY 1141 TTGACTACTGCTTTTATTTAATACAGTTTCAGAAACCCCTGAAGTTTAACTTCA 1200  
DB 1141 TTGACTACTGCTTTTATTTAATACAGTTTCAGAAACCCCTGAAGTTTAACTTCA 1200  
OY 1201 TTATCTTTAATACATTTGAGAGATGAGATGATGATGACAGGCTGGGGCAAGAA 1260  
DB 1201 TTATCTTTAATACATTTGAGAGATGAGATGATGATGACAGGCTGGGGCAAGAA 1260  
OY 1261 CAGGGGCACTAGCTGCTTATTAAGTATTTAGTCCCTCCGCTGTTAGCTTAACTTTG 1320  
DB 1261 CAGGGGCACTAGCTGCTTATTAAGTATTTAGTCCCTCCGCTGTTAGCTTAACTTTG 1320  
OY 1321 ACCCTTCTTTTATTCACAAAATACATTTAAACTGGAATTCATACAAATGCTATTT 1380  
DB 1321 ACCCTTCTTTTATTCACAAAATACATTTAAACTGGAATTCATACAAATGCTATTT 1380



Db 131 ACCCTTCCCTTTGATCCACAAATACATTAATACTGTAATTCACATACATGCTATT 1380  
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 Oy 1441 ATGTGCCCCCAGCAGTCCGCCCACTTGGATGCGGTCAGAGAGTTGAGTTGCTATT 1500  
 Db 1441 ATGTGCCCCCAGCAGTCCGCCCACTTGGATGCGGTCAGAGAGTTGAGTTGCTATT 1500  
 Oy 1501 AACCAATGTCATTAATATCTCTAGAGTACAGTGCATATATATCAATGTTGCTAG 1560  
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 Db 1561 TTGACACAGGATTTTATCTGAAGAATACATATTAATTAATACCTTAGAGAAAG 1620  
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 Oy 1681 ATTAACACACCTTTTCTTAAGTAAAAA 1712  
 Db 1681 ATTAACACACCTTTTCTTAAGTAAAAA 1712  
 RESULT 2  
 AA95787  
 ID AA95787 standard; cDNA: 1760 BP.  
 XX  
 AA95787;  
 DT 28-FEB-2001 (first entry)  
 XX  
 Human immune system molecule cDNA from Incyte clone 1890540.  
 DE  
 XX  
 Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianemic;  
 KW antiherpes; antileukemic; antidiabetic; nephrotoxic; cancer;  
 KW antiherpes; antileukemic; antidiabetic; nephrotoxic; cancer;  
 KW immunosuppressive; cytotoxic; fungicide; protozoicide; antibacterial;  
 KW gene therapy; diagnostic; immunological disorder; viral infection; ss;  
 KW bacterial infection; fungal infection; parasitic infection; immunogen.  
 OS  
 XX Homo sapiens.  
 XX  
 PN WO200006080-A2.  
 XX  
 PD 12-OCT-2000.  
 XX  
 PE 04-APR-2000; 2000WO-US09072.  
 XX  
 PR 05-APR-1999; 99US-0127852.  
 XX  
 PR 05-MAY-1999; 99US-0132647.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Yue H, Lal P, Tang YT, Baughn MR, Azimzai Y, Lu DM:  
 DR WPI: 2000-665005/64.  
 DR P-PSDB: AAB15548.  
 XX  
 PT New human immune system molecules 1-15 and polynucleotides encoding  
 PT them useful for diagnosing, treating or preventing e.g. immunological  
 PT disorders, infections, cell proliferative disorders, microbial  
 PT infections  
 PS  
 PS Claim 4: Page 93; 95pp; English.  
 CC  
 CC This sequence represents the cDNA for a human immune system molecule  
 CC (IMOL) isolated as clone 1890540 from the Incyte B1ADT07 library.  
 CC The human IMOLs (AAB15536-B15550) and their encoding polynucleotides  
 CC (AA95775-A95789), and compositions comprising them are useful for the

CC diagnosis, treatment or prevention of immunological disorders,  
 CC infections and cell proliferative disorders, including cancer. The IMOL  
 CC may be used to treat or prevent disorders associated with decreased  
 CC expression or activity of IMOL, such as immunological disorders  
 CC (e.g. inflammation, actinic keratosis, AIDS, Addison's disease),  
 CC haematopoietic cancer, infections caused by virus (e.g. adenovirus,  
 CC parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus,  
 CC Shigella), fungi (e.g. Aspergillus, Blastomyces), parasites (e.g.  
 CC Plasmodium, Trypanosoma, intestinal protozoa), cell proliferative  
 CC disorders (e.g. actinic keratosis, arteriosclerosis, buritis), and  
 CC cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also  
 CC useful as immunogens for the development of antibodies that  
 CC specifically recognize these peptides. The polynucleotides may be used  
 CC to detect and quantify gene expression in biopsied tissues in which  
 CC expression of IMOL may be correlated with the disease, as targets in a  
 CC microarray, to detect differences in gene sequences among normal,  
 CC carrier and affected individuals, and for screening libraries of  
 CC compounds in drug screening techniques. Antibodies which specifically  
 CC bind to IMOL may be used for the diagnosis of disorders characterized  
 CC by expression of IMOL, or in assays to monitor patients being treated  
 CC with IMOL or agonists, antagonists, or inhibitors of IMOL.  
 XX  
 SQ Sequence 1760 BP; 505 A; 376 C; 395 G; 484 T; 0 other:  
 Query Match 99.9%; Score 1710.4; DB 21; Length 1760;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1711; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 GGCATGCCCCGAGAGACACGCTCTGAGCTGCTGCTCTTCACAGGAGACTCTGA 60  
 Db 48 GGCATGCCCCGAGAGACACGCTCTGAGCTGCTGCTCTTCACAGGAGACTCTGA 107  
 Oy 61 GGCCTGTGAGATCAGCTTTGGAGGAGCTCATCTATTGAGCACTGCTGCTTTGTT 120  
 Db 108 GGCCTGTGAGATCAGCTTTGGAGGAGCTCATCTATTGAGCACTGCTGCTTTGTT 167  
 Oy 121 TTTCTCCCTTTTGGCTGTCAAGTAAATACATGAGTCTCCACAAACGGAGACT 180  
 Db 168 TTTCTCCCTTTTGGCTGTCAAGTAAATACATGAGTCTCCACAAACGGAGACT 227  
 Oy 181 ACCCCAGACTCAGTAAGTGTGTATGAGACTACACTTTCCAGGCTACCAAGCCC 240  
 Db 228 ACCCCAGACTCAGTAAGTGTGTATGAGACTACACTTTCCAGGCTACCAAGCCC 287  
 Oy 241 CCTGGGCGACGGGCGCTCTGGCATTCAGAAACCAATGAGAAATGGCAACATG 300  
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 Oy 301 AGCACTGCTCATGAAGAGCCAAAGTGAGAGGCGACAAAGTGACCTGGGCTCG 360  
 Db 348 AGCACTGCTCATGAAGAGCCAAAGTGAGAGGCGACAAAGTGACCTGGGCTCG 407  
 Oy 361 AGGGAGCGGGGCGACATGCGCCCAAGAGAGAGAGGCTACCCGGGATTCACACAG 420  
 Db 408 AGGGAGCGGGGCGACATGCGCCCAAGAGAGAGAGGCTACCCGGGATTCACACAG 467  
 Oy 421 ACTTCAGATTGATTCAGATGAGCTTCTGCAACCCACTTCAGAAATCAGAAAGTGGAT 480  
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 Oy 481 TATCTTCACAGTGTGAGAGCAACATTTGAAATCTTTGATGTCATGATGTTGATT 540  
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 Oy 541 TGGGGCCCCAGTACAGTGTGATTTCTTCACCTTCACAGTATACAGTATGAGATG 600  
 Db 588 TGGGGCCCCAGTACAGTGTGATTTCTTCACCTTCACAGTATACAGTATGAGATG 647  
 Oy 601 TGAGAGGTATGATGATCTTATGCAATGGCAACAGCTTATGAGATGAGAGCTA 660  
 Db 648 TGAGAGGTATGATGATCTTATGCAATGGCAACAGCTTATGAGATGAGAGCTA 707  
 Oy 661 TGAATGAGAGGCAATCAGATACATCCAGCAATCATGCTGTGCTAGAGCTACCAAG 720

[illegible]

| ID  | Accession  | Standard      | CDNA      | BP           |
|---|--|---------------|-----------|--------------|
| AA064058  | standard   | CDNA          | 1696      | BP           |
| AA064058  |  |               |           |              |
| AA064058  |  |               |           |              |
| 19-FEB-2001   | (first entry)  |               |           |              |
| Human zacr3p3   | CDNA, SEQ ID NO:1  |               |           |              |
| Human zacr3p3   | adipocyte complement related protein homologue; ACRP30; C1q domain; collagen-like domain; energy balance modulation; cellular metabolism; metabolic disorder; obesity; anorexia; antimicrobial agent; infection; platelet aggregation inhibition; adhesion; activation; vascular injury; antibacterial; antiviral; ss. |               |           |              |
| Homo sapiens  |  |               |           |              |
| MO200063377-A1  |  |               |           |              |
| 26-OCT-2000   |  |               |           |              |
| 19-APR-2000   | 2000WO-US10454   |               |           |              |
| 20-APR-1999   | 99US-0294943   |               |           |              |
| (ZYMO )   | ZYMOGENETICS INC.  |               |           |              |
| Piddington CS, Bishop PD  |  |               |           |              |
| WPI: 2000-665243/64   |  |               |           |              |
| P-PSDB: AAB29580  |  |               |           |              |
| Novel zacr3p3 polypeptides used to treat or prevent bacterial or viral infections for wound healing, improving blood flow, and to analyze energy efficiency in mammals  |  |               |           |              |
| Claim 31: Page 107-109; 123pp; English  |  |               |           |              |
| The invention relates to the human zacr3p3 protein (AAB29580) and to nucleic acids which encode it (AAC64058, AAC64063). Zacr3p3 is a homologue of adipocyte complement related protein (ACRP30) and contains a collagen-like domain comprising 10 beta-strands. The zacr3p3 gene is located on chromosome 5p12. The invention also relates to zacr3p3 fragments, fusion proteins containing zacr3p3 polypeptides, zacr3p3-specific antibodies, expression constructs and host cells comprising zacr3p3 nucleic acids, and methods of recombinant production of zacr3p3. Human zacr3p3, and its agonists and antagonists may be used in the study and modulation of cellular metabolism and energy balance in mammals, and may therefore be used to treat disorders such as obesity and anorexia, and conditions associated with these disorders. Due to its C1q like domain, zacr3p3 and zacr3p3-containing fusion proteins may be useful as antimicrobial agents, promoting lysis or phagocytosis of infectious organisms such as bacteria or viruses. Zacr3p3, its fragments, fusion proteins, antibodies and activity modulators may also be used to inhibit collagen induced platelet aggregation, adhesion, or activation, and may therefore have potential for promoting blood flow within the vasculature of a mammal e.g., to treat injury to the vasculature or other collagenous tissue. Human zacr3p3 and its antibodies may additionally be used to study dimerisation and oligomerisation. The present sequence represents CDNA encoding human zacr3p3. |  |               |           |              |
| Sequence 1696 BP; 482 A; 355 C; 386 G; 473 T; 0 other:  |  |               |           |              |
| Query Match   | 99.1%;   | Score 1696;   | DB 21;    | Length 1696; |
| Best Local Similarity   | 100.0%;  | Pred. No. 0;  |           |              |
| Matches 1696;   | Conservative 0;  | Mismatches 0; | Indels 0; | Gaps 0;      |
| 9   | CCCCGAGGAGACACAGCCTCTGGAGCTGTCGCTCTTCACGAGACACCTAGGCTCTGT  | 68            |           |              |
| 1   | CCCCGGGAGACACACCTCTGGAGCTCTGCGCTCTTCCTCAGGAGACACCTCAGGCTCTGT   | 60            |           |              |
| 59  | TGAGATATCATGCTTTGGAGGAGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTCTCC  | 128           |           |              |



XX Claim 1; SEQ ID 261; 609pp + CD ROM; English.  
PS

This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by AAB88317 - AAB88419. Included in the invention are primers AAF93917 - AAF94495 and AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies (agonists and antagonists) may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes.

Sequence 1709 BP; 480 A; 363 C; 390 G; 476 T; 0 other;

|                            |        |               |           |              |
|----------------------------|--------|---------------|-----------|--------------|
| Query Match                | 99.08; | Score 1695.4; | DB 22;    | Length 1709; |
| Best Local Similarity      | 99.98; | Pred. No. 0;  |           |              |
| Matches 1696; Conservative | 0;     | Mismatches 1; | Indels 0; | Gaps 0;      |

|    |     |  |     |
|----|-----|--|-----|
| OY | 1   | GGACATGCCCCGAGAGACCAAGCTCCTGGAGGCTGCTGTCCTTCTCAGGAGACACTGA     | 60  |
| Db | 13  | GGCATCTGCCCCGAGAGACCAAGCTCCTGGAGGCTGCTGTCCTTCTCAGGAGACACTGA    | 72  |
| OY | 61  | GGCTCTGTGGAAATCATAGCTTTTGGAGGACAGCTCATATTTGGCAATGCTGGCTTGT     | 120 |
| Db | 73  | GGCTCTGTGGAAATCATAGCTTTTGGAGGACAGCTCATATTTGGCAATGCTGGCTTGT     | 132 |
| OY | 121 | TTTCCCTCCCTTTTGGCTGTCTCAAGATGAATATACATGAGAGCTTCCACAAACGGAGACT  | 180 |
| Db | 133 | TTTCCCTCCCTTTTGGCTGTCTCAAGATGAATATACATGAGAGCTTCCACAAACGGAGACT  | 192 |
| OY | 181 | ACCCCCAGACAGCATGAAGTGTCTCATGAGAGACTAACGTTTTCGAGAGTACCAAGGCC    | 240 |
| Db | 193 | ACCCCCAGACAGCATGAAGTGTCTCATGAGAGACTAACGTTTTCGAGAGTACCAAGGCC    | 252 |
| OY | 241 | CCCTGGGACACCGGAGCCCTCCTGGCATTTCCAGAGAAACATGAGAAACATGGCAACATG   | 300 |
| Db | 253 | CCCTGGGACACCGGAGCCCTCCTGGCATTTCCAGAGAAACATGAGAAACATGGCAACATG   | 312 |
| OY | 301 | AGCCACTGCTCATGAAGGAGCCAAAGCTGAGAAAGGCGGACAAAGGTGACCTGGGGCCTCG  | 360 |
| Db | 313 | AGCCACTGCTCATGAAGGAGCCAAAGGTGAGAAAGGCGGACAAAGGTGACCTGGGGCCTCG  | 372 |
| OY | 361 | AGGGGAGCGGGGGGACGATGGCCCCCAAGAGAGAAAGGCTACCCGGGGATTCCACCAGA    | 420 |
| Db | 373 | AGGGGAGCGGGGGGACGATGGCCCCCAAGAGAGAAAGGCTACCCGGGGATTCCACCAGA    | 432 |
| OY | 421 | ACTTCAGATTTCATTCATGAGCTTCTCTGGCAACCCACTTCAGCAATATAGAAACAGTGGAT | 480 |
| Db | 433 | ACTTCAGATTTCATTCATGAGCTTCTCTGGCAACCCACTTCAGCAATATAGAAACAGTGGAT | 492 |
| OY | 481 | TATCTTCAGCAGTGTGAGACCAACATTTGAAACTTCTTTGATGTCTGAAGTGGATTT      | 540 |
| Db | 493 | TATCTTCAGCAGTGTGAGACCAACATTTGAAACTTCTTTGATGTCTGAAGTGGATTT      | 552 |
| OY | 541 | TGGGGCCCCAGTATTCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGATGT   | 600 |
| Db | 553 | TGGGGCCCCAGTATTCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGATGT   | 612 |

|    |      |   |     |
|----|------|---|-----|
| OY | 601  | TGAGGAACTGTAATGTGTACCTTAATGACAAATGGCACACACAGCTCTTCAAGCATGTACAGCTA | 660 |
| Db | 613  | TGAGAAATGTATGTGTATACCTTAATGACAAATGGCAACACAGCTCTTCAAGCATGTACAGCTA  | 672 |
| OY | 661  | TGAATTAAGAGGCAAAATACATATCATCTCAGCAATCATGTGTCTCAAGCTACCAAGG        | 720 |
| Db | 673  | TGAATTAAGAGGCAAAATACATATCATCTCAGCAATCATGTGTCTCAAGCTACCAAGG        | 732 |
| OY | 721  | GGATGAGGTTTTGGCTGCGAATGGGCAATGGGGCTTCCATGGGGACCACCAACGTTTCTC      | 780 |
| Db | 733  | GGATGAGGTTTTGGCTGCGAATGGGCAATGGGGCTCTCCATGGGGACCACCAACGTTTCTC     | 792 |
| OY | 781  | CACCTTTCAGAGATTCCTCGCTCTTTGAAACATAGTAATATATAGCTAGAAATAGCTCCAC     | 840 |
| Db | 793  | CACCTTTCAGAGATTCCTCGCTCTTTGAAACATAGTAATATATAGCTAGAAATAGCTCCAC     | 852 |
| OY | 841  | TTTTGGGGAAGACTGTATAGCTGAGCTGATTTGTATACGATCTGAGGAACATTTAAAGTTGAGG  | 900 |
| Db | 853  | TTTTGGGGAAGACTGTATAGCTGAGCTGATTTGTATACGATCTGAGGAACATTTAAAGTTGAGG  | 912 |
| OY | 901  | GTTTTACATTGCTGTATTCAAAAAATTATTGGTTGCATATGTTGTTCACGCTACAGGTACA     | 960 |
| Db | 913  | GTTTTACATTGCTGTATTCAAAAAATTATTGGTTGCATATGTTGTTCACGCTACAGGTACA     | 972 |
| OY | 961  | CCAATTAAGTGGGCAAAATTCAGGGGCTCAGAGAATACACAAAAATATCTTTCACGA         | 102 |
| Db | 973  | CCAATTAAGTGGGCAAAATTCAGGGGCTCAGAGAATACACAAAAATATCTTTCACGA         | 103 |
| OY | 1021 | TGACCTTGACTAATATATACACAGATCTTATACATCTTTCCTTGGCACCTTAAAGATTAAT     | 108 |
| Db | 1033 | TGACCTTGACTAATATATACACAGATCTTATATACATCTTTCCTTGGCACCTTAAAGATTAAT   | 109 |
| OY | 1081 | TCTCCTCAGACGAGGTGGAAAAATTTTTTTTCATACAGAAATCATTTGGCAAAAGATTT       | 114 |
| Db | 1093 | TCTCCTCAGACGAGGTGGAAAAATTTTTTTTCATACAGAAATCATTTGGCAAAAGATTT       | 115 |
| OY | 1141 | TTGACTACTGCTGTTTTAATTTAATPACAGATTTTCAGAGAACCCCTGAAGTTTAAAGTTCA    | 120 |
| Db | 1153 | TTGACTACTGCTGTTTTAATTTAATPACAGATTTTCAGAGAACCCCTGAAGTTTAAAGTTCA    | 121 |
| OY | 1201 | TTATTCTTTAATACATTTTGAGAGAAATGGGATGTATATGACAGGGCTGGGGCAAGAA        | 126 |
| Db | 1213 | TTATTCTTTAATACATTTTGAGAGAAATGGGATGTATATGACAGGGCTGGGGCAAGAA        | 127 |
| OY | 1261 | CAGGGGCACTAGCTGCCCTTATTACTAATTTAATGAGCCCTCGGTTACGTTAGCCCTTGG      | 132 |
| Db | 1273 | CAGGGGCACTAGCTGCCCTTATTACTAATTTAATGAGCCCTCGGTTACGTTAGCCCTTGG      | 133 |
| OY | 1321 | ACCCTTTCCTTTTGATCCACAAAAATACATTTAAACCTGTGAATTCACATACATGCTAATTT    | 138 |
| Db | 1333 | ACCCTTTCCTTTTGATCCACAAAAATACATTTAAACCTGTGAATTCACATACATGCTAATTT    | 139 |
| OY | 1381 | TAAATGCAATGATTTTAAGCTATATAAGGCGTTGACGAGTATGGTGTGAATTTGTGTG        | 144 |
| Db | 1393 | TAAATGCAATGATTTTAAGCTATATAAGGCGTTGACGAGTATGGTGTGAATTTGTGTG        | 145 |
| OY | 1441 | ATGTTTCCCCCACAATCGCCCCCAACTTGGAGTGGGGCTCAGAGAGTTGAAGTTTCACTAAT    | 150 |
| Db | 1453 | ATGTTTCCCCCACAATCGCCCCCAACTTGGAGTGGGGCTCAGAGAGTTGAAGTTTCACTAAT    | 151 |
| OY | 1501 | AACCAATGTCAATTAATATCTATAGAGGTACAGTGGCCATATAGATATTCCAATGTGTGCATG   | 156 |
| Db | 1513 | AACCAATGTCAATTAATATCTATAGAGGTACAGTGGCCATATAGATATTCCAATGTGTGCATG   | 157 |
| OY | 1561 | TTGACACAGAGGATTTTATCTGAAGAACATACACTATTAAATTAATACCTTGAGAGAAAG      | 162 |
| Db | 1573 | TTGACACAGAGGATTTTATCTGAAGAACATACACTATTAAATTAATACCTTGAGAGAAAG      | 163 |
| OY | 1621 | ATTTTGAACCTGGCTTTAGATTAACACTGTGGCAGAGAAAAATGTAAATGACAAATATATGAA   | 168 |
| Db | 1633 | ATTTTGAACCTGGCTTTAGATTAACACTGTGGCAGAGAAAAATGTAAATGACAAATATATGAA   | 169 |

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Oy 1681 ATAAACACACCTTTGTT 1697
    |||||
Db 1693 ATAAACACACCTTTGTT 1709

RESULT 5
AAI99523
ID AAI99523 standard; cDNA; 1620 BP.
XX
AC AAI99523;
XX
DT 07-JAN-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 21.
XX
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antinflammatory; antitumor;
KW vulnerrary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; Cancer; Immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; ss.
XX
OS Homo sapiens.
XX
PN WO20015173-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01356.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
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PR 30-JUN-2000; 2000US-0215135.
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PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
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PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225577.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
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PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
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PR 01-SEP-2000; 2000US-0229287.
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PR 05-SEP-2000; 2000US-0229513.
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PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0231413.
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PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
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PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235634.
PR 27-SEP-2000; 2000US-0235636.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
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PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244674.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
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PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
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PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249264.  
 PR 17-NOV-2000; 2000US-0249265.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249299.  
 PR 17-NOV-2000; 2000US-0249300.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 05-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251899.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

XX MPI: 2001-451924/48.

XX P-PSDB; AAM99925.

PT New nucleic acids and polypeptides, useful for treating, preventing or  
 DR ameliorating human disorders and diseases -  
 XX  
 PS Claim 1; SEQ ID NO 21; 465bp + Sequence Listing; English.

CC The invention relates to novel human polynucleotides (AA195513-AA195538)  
 CC and the encoded proteins (AAM9915-AAM9934) which are useful for  
 CC preventing, treating or ameliorating medical conditions e.g. by protein  
 CC or gene therapy. The genes are isolated from a range of human tissues  
 CC disclosed in the specification. The nucleic acids, proteins, antibodies  
 CC and (antagonists are useful in the diagnosis, treatment and prevention  
 CC of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the  
 CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,  
 CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,  
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,  
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid  
 CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as  
 CC myocardial ischaemia; (d) wound healing; (e) neurological diseases  
 CC e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as  
 CC viral, bacterial, fungal and parasitic infections.

CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).

XX Sequence 1620 BP; 485 A; 332 C; 360 G; 440 T; 3 other;

Query Match 90.5%; Score 1549.6; DB 22; Length 1620;

Best Local Similarity 99.7%; Pred. No. 0; Matches 1549; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 159 AGTCTCCAAACCGGAGACTACCCCGAGACTGAGTGTGTCATGAGACTACA 218  
 DB 22 AGTCTCCAAACCGGAGACTACCCCGAGACTGAGTGTGTCATGAGACTACA 81  
 OY 219 GCTTTCAGGTACCAAGGCCCCCGGCGACGCGGCCCTCCGCGATTCAGAGAAC 278  
 DB 82 GCTTTCAGGTACCAAGGCCCCCGGCGACGCGGCCCTCCGCGATTCAGAGAAC 141  
 OY 279 ATGGAACAATGCGACATGAGCCACTGTGTCATGAAGAGCCAAAGTGAGAGGCG 338  
 DB 142 ATGGAACAATGCGACATGAGCCACTGTGTCATGAAGAGCCAAAGTGAGAGGCG 201  
 OY 339 ACAAGGTGACCTGGGCGCTGAGGGGAGCGGGGAGCATGCGCCCAAGAGAGAGG 398  
 DB 202 ACAAGGTGACCTGGGCGCTGAGGGGAGCGGGGAGCATGCGCCCAAGAGAGAGG 261

OY 399 GCTACCCGGGATTCACACGAACTTCAGATTGATTCATGCTCTCTGCGAACCCACT 458  
 DB 262 GCTACCCGGGATTCACACGAACTTCAGATTGATTCATGCTCTCTGCGAACCCACT 321  
 OY 459 TCAGCAATCAGAACAGTGGGATTAATCTTCACAGAGTGTGAGACCAACATTTGGAATCTCT 518  
 DB 322 TCAGCAATCAGAACAGTGGGATTAATCTTCACAGAGTGTGAGACCAACATTTGGAATCTCT 381  
 OY 519 TTGATGTCATGACCTGGAGATTTGGGGCCCGCAGATACAGGATGTTATTTCTTCACCTTCA 578  
 DB 382 TTGATGTCATGACCTGGAGATTTGGGGCCCGCAGATACAGGATGTTATTTCTTCACCTTCA 441  
 OY 579 GCATGATGAAGCATGAGAGTGTGAGGAAGTGTATGTATACCTTATTCACAAATGGCAACA 638  
 DB 442 GCATGATGAAGCATGAGAGTGTGAGGAAGTGTATGTATACCTTATTCACAAATGGCAACA 501  
 OY 639 CAGTCTTCACATGTACAGCTATGAATGAAGGGCAATCAGATACATCCAGCAATCATG 698  
 DB 502 CAGTCTTCACATGTACAGCTATGAATGAAGGGCAATCAGATACATCCAGCAATCATG 561  
 OY 699 CTGTGCTGAAGCTAGCCCAAGGGGATGAGCTTGGCTGCCAATGGGGCAATGGCGCTCC 758  
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 DB 742 CTGAGGAACATTAAGTTGAGGGTTTACATGCTGATTTCAAAAATTAATGCTTGCAG 801  
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 DB 802 TGTGTTACAGCTCAGGTACCAATATATGTTGAGATTCAGGGCTCGAAGAAATCA 861  
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 DB 922 TCCCTGGCAGCTTAAGAATATTTCTCTCAGCAGGAGTGGAAATATTTTCTCTATCA 981  
 OY 1119 CAGAGTCATTTGGAAGAAATTTGAGTCTGCTTTTAAATTAATTAATCAAGTTTTCAGG 1178  
 DB 982 CAGAGTCATTTGGAAGAAATTTGAGTCTGCTTTTAAATTAATTAATCAAGTTTTCAGG 1041  
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 DB 1042 AACCCCTGAAGTTTAAAGTCAATTAATCTTTTAACAATTTGAGAGAAATCGAGTATGTA 1101  
 OY 1239 TATACACAGGCTGGGGGCAAGACAGGGGCACTAGCTGCTTATTAATTAATTAATGAGCC 1298  
 DB 1102 TATACACAGGCTGGGGGCAAGACAGGGGCACTAGCTGCTTATTAATTAATTAATGAGCC 1161  
 OY 1299 TCCGTTTACAGTACCTTGGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1358  
 DB 1162 TCCGTTTACAGTACCTTGGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1221  
 OY 1359 GAATTCACATCAATGCTATTTTAAAGTCAATTAATTAATTAATTAATTAATTAATTAAT 1418  
 DB 1222 GAATTCACATCAATGCTATTTTAAAGTCAATTAATTAATTAATTAATTAATTAATTAAT 1281  
 OY 1419 TAATGTGTTGATTTTGTATGTTTCCCGCAGATGCGCCCAATCGGATGAGGAGG 1478  
 DB 1282 TAATGTGTTGATTTTGTATGTTTCCCGCAGATGCGCCCAATCGGATGAGGAGG 1341  
 OY 1479 CAGGAGTGTGAGTTCACTATTAACAATGTCAATAATATCTATAGAGTACAGTGCAC 1538



|||||  
Db 1342 CAGAGAGTGTAGGTTGCTTAAACAAATGTCATTAATCTCATAGAGGTACAGTCCCA 1401  
QY 1539 ATGATATTTCAAAATGTTGCAATGTTGACACAGGAGATTATATCTGAGAACATACACTA 1598  
Db 1402 ATGATATTTCAAAATGTTGCAATGTTGACACAGGAGATTATATCTGAGAACATACACTA 1461  
QY 1599 TTATATAATCTTAAAGAAAGATTGTTGACCTGGCTTATATATAAAGTGGCAGAGAAA 1658  
Db 1462 TTATATAATCTTAAAGAAAGATTGTTGACCTGGCTTATATATAAAGTGGCAGAGAAA 1521  
QY 1659 ATGTAATGACCAATATATGGAATTAACACACCTTTGTTAAAGATMAAAAAA 1712  
Db 1522 ATGTAATGACCAATATATGGAATTAACACACCTTTGTTAAAGATMAAAAAA 1575  
RESULT 6  
AA159230 standard; cDNA: 1792 BP.  
AA159230:  
AC AA159230:  
XX  
XX 22-OCT-2001 (first entry)  
DE Human polynucleotide SEQ ID NO 1433.  
XX  
KM Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KM peripheral nervous system; neuropathy; central nervous system; CNS;  
KM Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic;  
KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KM chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KM Leukemia; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO20015312-A1.  
XX  
PD 26-JUL-2001.  
XX  
PF 26-DEC-2000; 2000MO-US34263.  
XX  
XX 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
PR 09-JUL-2000; 2000US-0598042.  
PR 19-JUL-2000; 2000US-0620312.  
PR 03-AUG-2000; 2000US-0653450.  
PR 14-SEP-2000; 2000US-0662191.  
PR 19-OCT-2000; 2000US-0693036.  
PR 29-NOV-2000; 2000US-0727344.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;  
PI Zhao QA, Zhou P, Goodrich R, Drmanac R;  
XX  
DR WPI: 2001-442253/47.  
DR P-PSDB: AAA40074.  
XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders  
XX such as central nervous system injuries -  
PS Claim 1; SEQ ID NO 1433; 10078bp; English.  
XX  
XX The invention relates to human nucleic acids (AA157798-AA161369) and  
CC the encoded polypeptides (AA158642-AA162213) with nootropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localized neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukemias and  
CC C.N.S disorders.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification.  
XX  
SQ Sequence 1792 BP; 541 A; 352 C; 393 G; 506 T; 0 other;  
Query Match 90.5%; Score 1548.6; DB 22; Length 1792;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1551; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 155 ATGAGCTCTCCACAAACCGGAGGACTACCCCAACAGTCAGTAGTGTTCATAGAGAC 214  
Db 238 AGGAGTCTCCACAAACCGGAGGACTACCCCAACAGTCAGTAGTGTTCATAGAGAC 297  
QY 215 TACAGCTTTGAGAGCTACCAAGGCCCTGGGACACCGGGCCCTCGTGGCATTCACAGA 274  
Db 298 TACAGCTTTGAGAGCTACCAAGGCCCTGGGACACCGGGCCCTCGTGGCATTCACAGA 357  
QY 275 AACCATGGAACCAATGAGCAACATGAGCCACCTGTCATGAAGGACCAAGGTGAGAA 334  
Db 358 AACCATGGAACCAATGAGCAACATGAGCCACCTGTCATGAAGGACCAAGGTGAGAA 417  
QY 335 GGGCACAAGGTGACCTGGGGCCCTCGAGGGGAGCGGGGGGACGACTGGCCCCCAAGAGAG 394  
Db 418 GGGCACAAGGTGACCTGGGGCCCTCGAGGGGAGCGGGGGGAGCGACTGGCCCCCAAGAGAG 477  
QY 395 AAGGCTACCCGGGGGATTCACACGAACTTCAGATTCATGAGTGTCTCTGGCAAC 454  
Db 478 AAGGCTACCCGGGGGATTCACACGAACTTCAGATTCATGAGTGTCTCTGGCAAC 537  
QY 455 CACTTCAGCAATGAAACAGTGGGATTAATCTTCAGACGTGTGAGACCAATTTGAAC 514  
Db 538 CACTTCAGCAATGAAACAGTGGGATTAATCTTCAGACGTGTGAGACCAATTTGAAC 597  
QY 515 TTCTTTATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 574  
Db 598 TTCTTTATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 657  
QY 575 TTTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 634  
Db 658 TTTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 717  
QY 635 AACACAGTCTTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 694  
Db 718 AACACAGTCTTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 777  
QY 695 CATGCTGTGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 754  
Db 778 CATGCTGTGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 837  
QY 755 CTCATGAGGAGACCAACAGCTTCTCCACCTTCAGAGATTCCTGCTTTGAACATGAG 814  
Db 838 CTCATGAGGAGACCAACAGCTTCTCCACCTTCAGAGATTCCTGCTTTGAACATGAG 897  
QY 815 TAAATATATGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 874  
Db 898 TAAATATATGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957  
QY 875 CGATCTGAGGAGACCTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 934  
Db 958 CGATCTGAGGAGACCTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1017  
QY 935 GCAATGTTGTTCAAGCTACAGGTACACCAATTAAGTTGAGCAATTCAGGGGCTCAGAGA 994  
Db 1018 GCAATGTTGTTCAAGCTACAGGTACACCAATTAAGTTGAGCAATTCAGGGGCTCAGAGA 1077  
QY 995 ATCAACCACAAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1054  
Db 1078 ATCAACCACAAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1137



OY 1055 TCTTTCCTTGGCACCATAAAGATATATTCCTCCCTGACGAGGTGGAAATATTTTTCCT 1114  
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 Db 1138 TCTTTCCTTGGCACCATAAAGATATATTCCTCCCTGACGAGGTGGAAATATTTTTCCT 1197  
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 OY 1115 ATCAGAGAAGTCATTGGCAAGAAATTTTGACTACTCTCTTTTAATTAATACAGTTT 1174  
 |||||||  
 Db 1198 ATCAGAGAAGTCATTGGCAAGAAATTTTGACTACTCTCTTTTAATTAATACAGTTT 1257  
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 OY 1175 CAGGAACCCCTGAGATTTTAAGTTCATTATTTTAACTTGAAGATTCGATGTA 1234  
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 Db 1258 CAGGAACCCCTGAGATTTTAAGTTCATTATTTTAACTTGAAGATTCGATGTA 1317  
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 OY 1235 GTGATATACAGGGCTGGGGCAGAGACAGGGGCTACTAGCTGCTTAATTAAGCAATTTTGT 1294  
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 Db 1318 GTGATATACAGGGCTGGGGCAGAGACAGGGGCTACTAGCTGCTTAATTAAGCAATTTTGT 1377  
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 OY 1295 GCCCTCCGTTTCACCTTACGCTTTGACCTTTCTCTTTGATCCAAATATACATTAATA 1354  
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 Db 1378 GCCCTCCGTTTCACCTTACGCTTTGACCTTTCTCTTTGATCCAAATATACATTAATA 1437  
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 Db 1438 CTCGATATTCACATACATGCTATTTTAAAGTCAATTAATTTTACCTTAATTAAGTCTTGA 1497  
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 OY 1415 CCAGTAATGTGGTGTATTTTGTGATGTCCTCCGACATGCCCCCACTTGGATGTG 1474  
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 OY 1475 GGGTCAGGAGGTGAGTTCCTACTATTAAACAATGCTAATTAATTCATAGAGTACAGT 1534  
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 OY 1535 GCCATATATATTTCAATGTTGCTGACCAAGAGGATTTTAATCTGAGAAACATAC 1594  
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 Db 1678 ACTATTAATTAATACCTTACAGAAAGATTTTGACCTGGCTTAAAGTAAACGTGGCAG 1737  
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 OY 1655 AAAAATGTATGAGCAATATATGAAATTAACACACCTTTGTTAAAGATTAATAA 1709  
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 Db 1738 AAAAATGTATGAGCAATATATGAAATTAACACACCTTTGTTAAAGATTAATAA 1792  
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 RESULT 7  
 AAD12584  
 ID AAD12584 standard; cDNA; 1927 BP.  
 XX  
 AC AAD12584;  
 XX  
 DT 25-SEP-2001 (first entry)  
 XX  
 DE Human protein having hydrophobic domain encoding cDNA clone HP10781.  
 XX  
 KW Human: hydrophobic domain; gene therapy; nutritional supplement;  
 cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;  
 multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;  
 haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;  
 Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;  
 haemostatic; thrombolytic; tumour growth inhibitor; anabolic;  
 contraceptive; antiinfertility; antiinflammatory; ss.  
 KW  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 89..760  
 FT /tag= a  
 FT /product= "Human protein having hydrophobic domain"  
 FT /note= "CDS is specifically is claimed in claim 3"  
 FT sig\_peptide 89..157  
 FT /\*tag= b

FT mat\_peptide 158..757  
 FT /\*tag= c  
 FT /product= "Mature human protein with hydrophobic domain"  
 XX  
 XX W0200149728-A2.  
 XX  
 XX 12-JUL-2001.  
 XX  
 XX 28-DEC-2000; 2000MO-JP09359.  
 XX  
 XX 06-JAN-2000; 2000JP-0000585.  
 XX  
 XX 06-JAN-2000; 2000JP-0000588.  
 XX  
 XX 11-JAN-2000; 2000JP-0002299.  
 XX  
 XX 03-FEB-2000; 2000JP-0026862.  
 XX  
 XX 03-MAR-2000; 2000JP-0058367.  
 XX  
 XX (PROT-) PROTEGENE INC.  
 XX (SAGA) SAGAMI CHEM RES CENT.  
 XX  
 XX Kato S, Kimura T;  
 XX  
 XX WPI: 2001-418355/44.  
 XX  
 XX P-PSDB: AAE06589.  
 XX  
 XX Human proteins with hydrophobic domains and the nucleic acids encoding  
 PT them, useful for preventing diagnosing and treating e.g. cancer.  
 PT Alzheimer's and inflammation -  
 PT  
 XX  
 XX Claim 4; Page 352-354; 563pp; English.  
 XX  
 XX The present sequence is human protein with hydrophobic domain encoding  
 CC cDNA clone HP10781. The polynucleotide and polypeptide of the invention  
 CC may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate polypeptide expression. The polynucleotides  
 CC may be used to produce the polypeptide, by inserting the nucleic acids  
 CC into a host cell and culturing the cell to express the protein. The  
 CC polynucleotides and its complementary sequences may also be used as DNA  
 CC probes in diagnostic assays and also used in gene therapy. The  
 CC polypeptides may also be used as antigens in the production of antibodies  
 CC and in assays to identify modulators of polypeptide expression and  
 CC activity. The polypeptides and nucleic acids may be used as nutritional  
 CC supplements, to modulate cytokine and cell proliferation activity, to  
 CC modulate immune stimulation or suppression (e.g. for the treatment of  
 CC microbial infections and autoimmune disorders such as multiple sclerosis,  
 CC rheumatoid arthritis and insulin-dependent diabetes), to modulate  
 CC haematopoiesis, to modulate tissue growth activity (e.g. for the  
 CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's  
 CC disease), to modulate activin and inhibin activity (e.g. for controlling  
 CC fertility), to modulate chemotactic and chemokinetic activity, to  
 CC modulate haemostatic and thrombolytic activity, to modulate receptor  
 CC ligand activity, to modulate inflammation and to inhibit tumour growth.  
 CC  
 XX  
 XX Sequence 1927 BP; 550 A; 416 C; 452 G; 509 T; 0 other;  
 XX  
 XX Query Match 89.2%; Score 1527; DB 22; Length 1927;  
 XX Best Local Similarity 99.9%; Pred. No. 0;  
 XX Matches 1538; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 OY 159 AGTCTCCACAAACCGGAGACTACCCCGACAGTCAGTAAGTGTGATGAGACTACA 218  
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 Db 390 AGTCTCCACAAACCGGAGACTACCCCGACAGTCAGTAAGTGTGATGAGACTACA 449  
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 OY 219 GCTTTCGAGGCTACCAAGGCCCTCGGCGACCGGGCCCTCGGCAATTCAGGAAC 278  
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 Db 450 GCTTTCGAGGCTACCAAGGCCCTCGGCGACCGGGCCCTCGGCAATTCAGGAAC 509  
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 OY 279 ATGGAACAAATGGAACATGAGGACACTGTCATGAAGAGCCAAAGGTGAGAGGCG 338  
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 Db 510 ATGGAACAAATGGAACATGAGGACACTGTCATGAAGAGCCAAAGGTGAGAGGCG 569  
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 OY 339 ACAAGGTCACCTGGGCTCGAGGGGAGCGGGGGCAGCAGTGGCCCAAAGGAGAAAG 398  
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 Db 570 ACAAGGTCACCTGGGCTCGAGGGGAGCGGGGGCAGCAGTGGCCCAAAGGAGAAAG 629  
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QY 399 GCTACCCGGGATTCACACGAACTTCAGATTCATGCTCTCTGGCAACCCACT 458  
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 Db 630 GCTACCCGGGATTCACACGAACTTCAGATTCATGCTCTCTGGCAACCCACT 689  
 QY 459 TCAGCAATCAGAACAGTGGGATTATCTTCAGAGTGTGGACCAACATTTGAACCTCT 518  
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 Db 690 TCAGCAATCAGAACAGTGGGATTATCTTCAGAGTGTGGACCAACATTTGAACCTCT - 748  
 QY 519 TTGATGTCACTGATGTTAGTTGGGGCCCATATCAGTGTGTATTTCTTCCACTTCA 578  
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 Db 749 TTGATGTCACTGATGTTAGTTGGGGCCCATATCAGTGTGTATTTCTTCCACTTCA 808  
 QY 579 GCATGATGAAGCATGATGAGATGTTGAGAAATGATGTACTTATGACACAAATGGCACA 638  
 |||||||  
 Db 809 GCATGATGAAGCATGATGAGATGTTGAGAAATGATGTACTTATGACACAAATGGCACA 868  
 QY 639 GAGTCTTCAGACATGATCAGATATGAAATGAAAGGCAAAATCAGATACATCCAGCAATCATG 698  
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 Db 869 CAGTCTTCAGACATGATCAGATATGAAATGAAAGGCAAAATCAGATACATCCAGCAATCATG 928  
 QY 699 CTGTGCTGAAGCTAGCCAAAGGGGATGAGTTGGCTGCGCAATGGGCAATGGCGCTCTCC 758  
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 Db 929 CTGTGCTGAAGCTAGCCAAAGGGGATGAGTTGGCTGCGCAATGGGCAATGGCGCTCTCC 988  
 QY 759 ATGGGACACCAACAGCTTCTCCACCTTTGACAGATTCCTGCTCTTGAAGACTAGTAA 818  
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 Db 989 ATGGGACACCAACAGCTTCTCCACCTTTGACAGATTCCTGCTCTTGAAGACTAGTAA 1048  
 QY 819 TATATGACTAGAAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGTATTTGTTACAT 878  
 |||||||  
 Db 1049 TATATGACTAGAAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGTATTTGTTACAT 1108  
 QY 879 CTAGAGCACTTAAATGATGGGCTTTTACATGCTGTATTCAAAATAATTTATGTTCCAA 938  
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 Db 1109 CTAGAGCACTTAAATGATGGGCTTTTACATGCTGTATTCAAAATAATTTATGTTCCAA 1168  
 QY 939 TGTGTTCACGCTACAGTGTACACCAATATGTTGGACAAATTCAGGGGCTCAGAAAGATCA 998  
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 Db 1169 TGTGTTCACGCTACAGTGTACACCAATATGTTGGACAAATTCAGGGGCTCAGAAAGATCA 1228  
 QY 999 ACCACAAATATGCTTCTCAGATGACCTTGAATATCTACTCAGACATCTTATCAGCTT 1058  
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 Db 1229 ACCACAAATATGCTTCTCAGATGACCTTGAATATCTACTCAGACATCTTATCAGCTT 1288  
 QY 1059 TCCTTGGCAGCTTAAAGATATCTCTCTGAGCGAGCTTGGAAATATTTTCTCTATCA 1118  
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 Db 1289 TCCTTGGCAGCTTAAAGATATCTCTCTGAGCGAGCTTGGAAATATTTTCTCTATCA 1348  
 QY 1119 CAGAAGCATTTGCAAGAAATTTGACTACTCTCTTTTATTTAATNCCAGTTTTCAGG 1178  
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 Db 1349 CAGAAGCATTTGCAAGAAATTTGACTACTCTCTTTTATTTAATNCCAGTTTTCAGG 1408  
 QY 1179 AACCCCTGAAGTTTAAATTCATATTTCTTATTAACATTTGAGAGAAATCGAGATAGTGA 1238  
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 Db 1409 AACCCCTGAAGTTTAAATTCATATTTCTTATTAACATTTGAGAGAAATCGAGATAGTGA 1468  
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 QY 1299 TCGGTGTTCAGCTTAGCTTGAACCTTTCCTTCTTGTATCCAAATAATATTAACCTCT 1358  
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 Db 1529 TCGGTGTTCAGCTTAGCTTGAACCTTTCCTTCTTGTATCCAAATAATATTAACCTCT 1588  
 QY 1359 GAATTCACATACATGCTATTTTAAAGTCAATAGATTTTAAAGTCTTAAAGTCTTGACAG 1418  
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 Db 1589 GAATTCACATACATGCTATTTTAAAGTCAATAGATTTTAAAGTCTTAAAGTCTTGACAG 1648  
 QY 1419 TAATGTGTTGTATTTTGTGTATGTTCCGCCACATCGCCCAACTTGGATGGGCT 1478  
 |||||||  
 Db 1649 TAATGTGTTGTATTTTGTGTATGTTCCGCCACATCGCCCAACTTGGATGGGCT 1708

QY 1479 CAGGAGCTTGAGGCTCAGTATTTAACAATGCTCATTAATATCTCAGAGCTACAGTCCCA 1538  
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 Db 1709 CAGGAGCTTGAGGCTCAGTATTTAACAATGCTCATTAATATCTCAGAGCTACAGTCCCA 1768  
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 Db 1769 ATGATATTTCAATGTTGGCATGTTGACCCAGAGGATTTTATCTGGAAGCAATACACTA 1828  
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 Db 1829 TTATATTAATACCTTAGAGAAAGATTTTGACCTGCTTTACATATAAACTGTGGCAAGAAA 1888  
 QY 1659 ATGTAATGAGCAATATATGGAATTAACACACCTTTGTT 1697  
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 Db 1889 ATGTAATGAGCAATATATGGAATTAACACACCTTTGTT 1927

RESULT 8  
 ABK35221  
 ID ABK35221 standard; cDNA; 1608 BP.  
 XX  
 AC ABK35221:  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE Human cDNA encoding secreted protein #359.  
 XX  
 KW Human; secreted protein; gene; ss: nutritional supplement; haemophilia;  
 KW Viral Infection; Bacterial Infection; fungal infection; diabetes; asthma;  
 KW autoimmune disorder; Rheumatoid arthritis; multiple sclerosis; tumour;  
 KW autoimmune thyroiditis; allergic reaction; neurodegenerative disease;  
 KW Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer;  
 KW coagulation disorder; inflammatory disorder; Crohn's disease; incision;  
 KW tissue regeneration; wound healing; burn; haematopoiesis;  
 KW myeloid cell deficiency; lymphoid cell deficiency.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200177288-A2.  
 PD 18-OCT-2001.  
 XX  
 PF 29-MAR-2001: 2001WO-0510224.  
 XX  
 PR 06-APR-2000: 2000US-195582P.  
 XX  
 PA (GEMT ) GENETICS INST INC.  
 XX  
 PI Wong GC, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;  
 XX Gulukota K, Graham JR;  
 XX WPI: 2002-179321/23.  
 DR  
 XX  
 XX Five hundred and ninety two polynucleotides derived from a variety of  
 PT human tissue sources which encode secreted proteins, useful for  
 PT treating immune deficiencies and disorders such as autoimmune disorders  
 PT  
 XX  
 PS Claim 1; Page 261-262; 372pp; English.  
 PS  
 CC The invention relates to 592 polynucleotides which have been derived from  
 CC a variety of human tissue sources and which encode novel secreted  
 CC proteins. The polynucleotides can be used as probes for the  
 CC identification and isolation of full length cDNA and genomic DNA. The  
 CC polynucleotides and proteins can also be used as nutritional supplements.  
 CC The proteins are useful in the treatment of various immune deficiencies  
 CC and disorders such as viral infections, bacterial infections, fungal  
 CC infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple  
 CC sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions  
 CC and conditions (e.g. asthma). They are also useful for treating  
 CC neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's  
 CC disease), liver fibrosis, coagulation disorders (e.g. haemophilia),  
 CC inflammatory disorders (e.g. Crohn's disease) and tumours. They are also

CC useful for tissue regeneration, for wound healing and in the treatment of  
 CC burns, incisions and ulcers. The proteins are also useful for regulating  
 CC haematopoiesis and for treating myeloid or lymphoid cell deficiencies.  
 CC Sequences ABK34863-ABK35454 represent polynucleotides of the invention.  
 XX

Sequence 1608 BP: 487 A; 305 C; 339 G; 477 T; 0 other;

Query Match 79.68; Score 1363.2; DB 24; Length 1608;  
 Best Local Similarity 99.88; Pred. No. 0;  
 Matches 1365; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 337 CGACAAAGGTACCTGGGGCTCGAGGGAGCGGGGAGCAGCCGCCCAAGAGAGAGAA 396
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QY 397 GGGGTACCCGGGGATTCACAGAACTTCAGATTGCATTCAGCTTCTCTGSCACCCA 456
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Db 61 GGGGTACCCGGGGATTCACAGAACTTCAGATTGCATTCAGCTTCTCTGSCACCCA 120
QY 457 CTTGAGCAATGAGAAAGTGGGATTAATCTGAGAGTGTGAGCAACCAATGGAATCTT 516
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Db 121 CTTGAGCAATGAGAAAGTGGGATTAATCTGAGAGTGTGAGCAACCAATGGAATCTT 180
QY 517 CTTGAGTGTGAGTGTGATTTGGGGCCCGAGTATCAGGTGTGATTTCTTCACTT 576
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Db 181 CTTGAGTGTGAGTGTGATTTGGGGCCCGAGTATCAGGTGTGATTTCTTCACTT 240
QY 577 CAGCATGATGAGCATGAGATGTTGAGGAAGTATGTACTTATGCAAAATGSCAA 636
    |||||||
Db 241 CAGCATGATGAGCATGAGATGTTGAGGAAGTATGTACTTATGCAAAATGSCAA 300
QY 637 CACAGTCTTCAGCATGTACACTATGAAATGAAGGCAAAACATATACATCCACATCA 696
    |||||||
Db 301 CACAGTCTTCAGCATGTACACTATGAAATGAAGGCAAAACATATACATCCACATCA 360
QY 697 TGCCTGCTGAGCTAGCCAAAGGGGATGAGTTGGCTGCGAATGGGCAATGGCGCT 756
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Db 361 TGCCTGCTGAGCTAGCCAAAGGGGATGAGTTGGCTGCGAATGGGCAATGGCGCT 420
QY 757 CCATGGGAGCACCAACAGCTTCTCCACTTTCAGAGATTCCTGCTTTGAAACTAAGTA 816
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Db 421 CCATGGGAGCACCAACAGCTTCTCCACTTTCAGAGATTCCTGCTTTGAAACTAAGTA 480
QY 817 AATATATACAGAAATAGCTCCACTTTGGGGAACATGTGTGCTGAGCTGATTTGTAAG 876
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Db 481 AATATATACAGAAATAGCTCCACTTTGGGGAACATGTGTGCTGAGCTGATTTGTAAG 540
QY 877 ATCTGAGGAGACATTAAGTTGAGGTTTATACATGTGTATTTCAAAAATATATGTTGC 936
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Db 541 ATCTGAGGAGACATTAAGTTGAGGTTTATACATGTGTATTTCAAAAATATATGTTGC 600
QY 937 AATGTTGTTACGCTTACAGGTACCAACAAATATGTTGCAAAATTCAGGGGCTCAGAGAAAT 996
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Db 601 AATGTTGTTACGCTTACAGGTACCAACAAATATGTTGCAAAATTCAGGGGCTCAGAGAAAT 660
QY 997 CAACCAACAATATAGCTCTCAGATGACCTGACTAATATCTCAGACATCTTTATCCTC 1056
    |||||||
Db 661 CAACCAACAATATAGCTCTCAGATGACCTGACTAATATCTCAGACATCTTTATCCTC 720
QY 1057 TTTCTTGGACCTTAAAGATATATTCCTCTGACGAGGTGGAATATATTTTCTAT 1116
    |||||||
Db 721 TTTCTTGGACCTTAAAGATATATTCCTCTGACGAGGTGGAATATATTTTCTAT 780
QY 1117 CACGAGAGTCAATTTGCAAGATTTTGCATCTGCTTTAATTAATACAGATTTTCA 1176
    |||||||
Db 781 CACGAGAGTCAATTTGCAAGATTTTGCATCTGCTTTAATTAATACAGATTTTCA 840
QY 1177 GGAACCCCTGAGATTTTATGATCTTATTTATACATTTGAGAAATGAGATAGT 1236
    |||||||
Db 841 GGAACCCCTGAGATTTTATGATCTTATTTATACATTTGAGAAATGAGATAGT 900
QY 1237 GATATGACAGGGCTGGGCAAGAACAGGGGCACTAGCTTATTTAGTAAATTAAGTGC 1296
    |||||||

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Db 901 GATATGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTTCCTTATTAATTAATTAAGTGC 960
QY 1297 CTTCCGTTGTCAGCTTACCTTTGACCTTCTTATGATCCACAAATTAATTAATTAAGTGC 1356
    |||||||
Db 961 CTTCCGTTGTCAGCTTACCTTTGACCTTCTTATGATCCACAAATTAATTAATTAAGTGC 1020
QY 1357 CTGAATTCACATTAATATCTTATTAAGTCAATTAATTAATTAATTAATTAATTAAGTGC 1416
    |||||||
Db 1021 CTGAATTCACATTAATATCTTATTAAGTCAATTAATTAATTAATTAATTAATTAAGTGC 1080
QY 1417 AGTAATGTTGTTAATTTTGTATGTTCCCAACATGCCCCCACTTGGATGTTGGG 1476
    |||||||
Db 1081 AGTAATGTTGTTAATTTTGTATGTTCCCAACATGCCCCCACTTGGATGTTGGG 1140
QY 1477 GTCAGAGGTTGAGGTTTACATTAATTAATTAATTAATTAATTAATTAATTAATTAAGTGC 1536
    |||||||
Db 1141 GTCAGAGGTTGAGGTTTACATTAATTAATTAATTAATTAATTAATTAATTAATTAAGTGC 1200
QY 1537 CAATGATATTCATTAATGTTGATGTTGACAGAGGATTTTATATCTGAGAAATATAC 1596
    |||||||
Db 1201 CAATGATATTCATTAATGTTGATGTTGACAGAGGATTTTATATCTGAGAAATATAC 1260
QY 1597 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAGTGC 1656
    |||||||
Db 1261 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAGTGC 1320
QY 1657 AAATGTAATGAGCAATATATGGAATTAACACACCTTTGTTAAGATA 1704
    |||||||
Db 1321 AAATGTAATGAGCAATATATGGAATTAACACACCTTTGTTAAGATA 1368

```

RESULT 9  
 AA161016/c  
 ID AA161016 standard; cDNA: 1799 BP.  
 XX  
 AA161016;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Human polynucleotide SEQ ID NO 5005.  
 XX  
 KW Human; neotropic; immunosuppressant; cytosolic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Sny-Draeger Syndrome; Chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO20015312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PE 26-DEC-2000; 2000WO-US34263.  
 XX  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-052317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0683036.  
 PR 29-NOV-2000; 2000US-0727344.  
 XX  
 PA (HXSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
 XX  
 DR WPI: 2001-442253/47.  
 DR P-PSDB: AAM41860.

XX Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -

PS Claim 1: SEQ ID NO 5005; 10078bp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and  
 CC the encoded polypeptides (AA158642-AA162213) with neurotrophic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.

XX Sequence 1799 BP; 531 A; 389 C; 344 G; 535 T; 0 other:

Query Match 75.7%; Score 1295.4; DB 22; Length 1799;  
 Best Local Similarity 93.6%; Pred. No. 0;  
 Matches 1401; Conservative 0; Mismatches 1; Indels 95; Gaps 1;

QY 303 CCACGTGTCATGAAGAGCCAAAGGTGAGAGGCGCAAAAGGTGACCTGGGCGCTCGAG 362  
 DB 1799 CCACGTGTCATGAAGAGCCAAAGGTGAGAGGCGCAAAAGGTGACCTGGGCGCTCGAG 1740  
 QY 363 GGGAGGGGGGGGAGCATGGCCCCCAAGAGAGAGAGGGGCTTACCGGGGATCCACCGAAG 422  
 DB 1739 GGGAGGGGGGGGAGCATGGCCCCCAAGAGAGAGAGGGGCTTACCGGGGATCCACCGAAG 1680  
 QY 423 TT----- 424  
 DB 1679 TTCAGGCTGGAGTGCAGTGTGTGATCTTGGCTACCTGCACCAAGGTTCAGC 1620  
 QY 425 -----CAGATTGCATTATGGCTTCT 447  
 DB 1619 GATTCTTGGCTCAACCTCTGGAGTAGCTGGGATTACAGATTGCATTATGGCTTCTCT 1560  
 QY 448 GGAACCCACTTACGAAATCAGAACAGTGGGATTATCTTACAGAGTGTAGACCAACAT 507  
 DB 1559 GGAACCCACTTACGAAATCAGAACAGTGGGATTATCTTACAGAGTGTAGACCAACAT 1500  
 QY 508 TGGAACTCTTGTATGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 567  
 DB 1499 TGGAACTCTTGTATGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
 QY 568 CTTTACCTTTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 627  
 DB 1439 CTTTACCTTTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
 QY 628 CAATGCAACACAGTCTTACAGCTATGACATGTAAGAAATTAAGGCAAAATCAGATACATC 687  
 DB 1379 CAATGCAACACAGTCTTACAGCTATGACATGTAAGAAATTAAGGCAAAATCAGATACATC 1320  
 QY 688 CAGCATCATGCTGTGCTGTAAGTACGCAAAAGGGGATGAGTTGGCTGGCAATGGGCAA 747  
 DB 1319 CAGCATCATGCTGTGCTGTAAGTACGCAAAAGGGGATGAGTTGGCTGGCAATGGGCAA 1260  
 QY 748 TGGCGCTTCATGAGGAGCCACCAAGCTTCTCACCTTTCAGAGATTCTGCTTTTGA 807  
 DB 1259 TGGCGCTTCATGAGGAGCCACCAAGCTTCTCACCTTTCAGAGATTCTGCTTTTGA 1200  
 QY 808 AACTAAGTAATATATGACTAGATAGCTCCTCTTGGGAAAGACTTGTAGCTGAGCTGA 867  
 DB 1199 AACTAAGTAATATATGACTAGATAGCTCCTCTTGGGAAAGACTTGTAGCTGAGCTGA 1140

QY 868 TTTGTACATCTGAGACATTAAGATTGAGGCTTTTACATTGCTGTATTCAAAAATT 927  
 DB 1139 TTTGTACATCTGAGACATTAAGATTGAGGCTTTTACATTGCTGTATTCAAAAATT 1080  
 QY 928 ATTGGTTGCAATCTGTGTCAGCTACAGGATACCAATATGTTGGACATTAGGGGCT 987  
 DB 1079 ATTGGTTGCAATCTGTGTCAGCTACAGGATACCAATATGTTGGACATTAGGGGCT 1020  
 QY 988 CAGAGATATCAACCAAAATATCTTTCAGATGACCTTGATTAATATACAGCATCT 1047  
 DB 1019 CAGAGATATCAACCAAAATATCTTTCAGATGACCTTGATTAATATACAGCATCT 960  
 QY 1048 TTATCACTCTTCTTGGCACTTAAAGATATTTCTCTGACGAGGTGGAATATT 1107  
 DB 959 TTATCACTCTTCTTGGCACTTAAAGATATTTCTCTGACGAGGTGGAATATT 900  
 QY 1108 TTTTTCATACAGAAATCTTTGCAAGAAATTTGACTCTCTGCTTTAATTATATAC 1167  
 DB 899 TTTTTCATACAGAAATCTTTGCAAGAAATTTGACTCTCTGCTTTAATTATATAC 840  
 QY 1168 CAGTTTTCAGAACCCCTGAAGTTTAAAGTTCATTTATTTTAACTTTGAGAGATC 1227  
 DB 839 CAGTTTTCAGAACCCCTGAAGTTTAAAGTTCATTTATTTTAACTTTGAGAGATC 780  
 QY 1228 GGATGTAGTATATGACAGGCTGGGGCAAGAACAGGGGCTAGCTGCTTTATAGCTA 1287  
 DB 779 GGATGTAGTATATGACAGGCTGGGGCAAGAACAGGGGCTAGCTGCTTTATAGCTA 720  
 QY 1288 ATTATAGCCCCCTCGTTCAGCTTACCTTACCTTACCTTTCCTTTGATTCACAAAAATAC 1347  
 DB 719 ATTATAGCCCCCTCGTTCAGCTTACCTTACCTTTCCTTTGATTCACAAAAATAC 660  
 QY 1348 ATTAAACTCTGAATTCATATCAATATCAATATCAATATCAATATCAATATCAATATCAAT 1407  
 DB 659 ATTAAACTCTGAATTCATATCAATATCAATATCAATATCAATATCAATATCAATATCAAT 600  
 QY 1408 TGCCTGACAGTAATGTGTTGTAATTTGTATGATGTTCCCAATCGCCCAACTTC 1467  
 DB 599 TGCCTGACAGTAATGTGTTGTAATTTGTATGATGTTCCCAATCGCCCAACTTC 540  
 QY 1468 GGATGTGGGCTCAGAGAGTTCAGCTTACATTAATCAAAATGATTAATATCTCATAGAG 1527  
 DB 539 GGATGTGGGCTCAGAGAGTTCAGCTTACATTAATCAAAATGATTAATATCTCATAGAG 480  
 QY 1528 GTACAGTGGCAATATGATTAATCAATATGTTGATGTTGACAGAGGATTTTATATCTGAAG 1587  
 DB 479 GTACAGTGGCAATATGATTAATCAATATGTTGATGTTGACAGAGGATTTTATATCTGAAG 420  
 QY 1588 AACATACATTAATTAATTAATACCTTAGAGAAAGATTTTGAACCTTGTAGATTAACCTG 1647  
 DB 419 AACATACATTAATTAATTAATACCTTAGAGAAAGATTTTGAACCTTGTAGATTAACCTG 360  
 QY 1648 TGGCAACAAAATTAATGAGCAATATATGGAATTAACACACCTTGTAAAGATA 1704  
 DB 359 TGGCAACAAAATTAATGAGCAATATATGGAATTAACACACCTTGTAAAGATA 303

RESULT 10  
 AAF94076  
 ID AAF94076 standard; DNM: 810 BP.  
 AC AAF94076;  
 DT 23-MAY-2001 (first entry)  
 XX  
 XX  
 DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 510.  
 XX  
 XX Human; secretory protein; membrane protein; vaccine; gene therapy;  
 KW rheumatoid arthritis; diabetes; PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN EP1067182-A2.

XX 10-JAN-2001.  
PD  
XX 07-JUL-2000; 2000EP-0114090.  
XX  
XX 08-JUL-1999; 99JP-0194179.  
PR 11-JAN-2000; 2000JP-0118775.  
PR 02-MAY-2000; 2000JP-0183766.  
XX  
XX (HELI-) HELIX RES INST.  
PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
XX WPI; 2001-093989/11.  
DR  
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in  
PT gene therapy or as candidate target molecules in drug development -  
XX  
PS Claim 4; SEQ ID 510; 609pp + CD ROM; English.  
XX  
XX This invention relates to nucleic acid sequences AAF93744 - AAF93916  
CC which encode human secretory or membrane proteins represented by  
CC AAB88317 - AAB88419. Included in the invention are primers  
CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the  
CC cDNA sequences of the invention. The invention also includes methods for  
CC the production of antibodies directed against the proteins, and cDNA  
CC sequences, which can be used in vaccines. The polynucleotide sequences  
CC can be used in gene therapy. The polynucleotide sequences and the  
CC proteins they encode may be used in the prevention, treatment and  
CC diagnosis of diseases associated with inappropriate secretory  
CC protein/membrane protein expression. The nucleic acids and complementary  
CC sequences may also be used as DNA probes in diagnostic assays  
CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the  
CC presence of similar nucleic acid sequences in samples. They may also be  
CC used to study the expression and function of secretory proteins/membrane  
CC polypeptides and their role in metabolism. The polypeptides may be used  
CC as antigens in the production of antibodies against them and in assays to  
CC identify modulators (agonists and antagonists) of expression and  
CC activity. The antibodies and antagonists may also be used as therapeutic  
CC agents to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of the  
CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay  
CC (ELISA). Examples of diseases which may be treated include rheumatoid  
CC arthritis and diabetes.  
XX  
XX  
SQ Sequence 810 BP; 200 A; 201 C; 218 G; 188 T; 3 other:  
Query Match 44.8%; Score 766.6; DB 22; Length 810;  
Best Local Similarity 98.9%; Pred. No. 1.3e-212;  
Matches 791; Conservative 0; Mismatches 7; Indels 2; Gaps 2;  
OY 1 GGCATCTGCCCGAGAGACCAACGCTCTCGAGCTGCTGCTTCTTCAGGAGACTCTGA 60  
DB 13 GGCATCTGCCCGAGAGACCAACGCTCTCGAGCTGCTGCTTCTTCAGGAGACTCTGA 72  
OY 61 GGCCTGTGTGAGATCAATGCTTTGGAGGAGCTCATATGGAACCTGAGCTTGT 120  
DB 73 GGCCTGTGTGAGATCAATGCTTTGGAGGAGCTCATATGGAACCTGAGCTTGT 132  
OY 121 TTTCTCCCTTTTTCCTGCTCAAGATGATATACATGAGAGTCTCCACAAACCGGAGACT 180  
DB 133 TTTCTCCCTTTTTCCTGCTCAAGATGATATACATGAGAGTCTCCACAAACCGGAGACT 192  
OY 181 ACCCCAGAGTGCAGTAAGTGTGTCTCATGAGACTACAGCTTTCAGAGCTACCAAGCCC 240  
DB 193 ACCCCAGAGTGCAGTAAGTGTGTCTCATGAGACTACAGCTTTCAGAGCTACCAAGCCC 252  
OY 241 CCTGTGGGACACGGGCTCTCGCATTTCCAGGAACCATGGGAACAATGGCAACAATGG 300  
DB 253 CCTGTGGGACACGGGCTCTCGCATTTCCAGGAACCATGGGAACAATGGCAACAATGG 312  
OY 301 AGCCACTGTGTCATGAAGAGCAAAAGGTGAGAGAGGACAAAGGTGACCTGGGGCTCG 360  
|||||

DB 313 AGCCACTGTGTCATGAAGAGCAAAAGGTGAGAGAGGCGCACAAAGGTGACCTGGGGCTCG 372  
OY 361 AGGGAGCGGGGGGAGCATGCGCCCAAGAGAGAGAGAGGCTACCGGGGATTCCACACA 420  
DB 373 AGGGAGCGGGGGGAGCATGCGCCCAAGAGAGAGAGGCTACCGGGGATTCCACACA 432  
OY 421 ACTTCAGATTCATCATGAGGCTTCTCTGAGCAACCCACATTCACATCAAGAGGGGAT 480  
DB 433 ACTTCAGATTCATCATGAGGCTTCTCTGAGCAACCCACATTCACATCAAGAGGGGAT 492  
OY 481 TATCTTCAGAGTGTGAGACCAACATTCGAACCTTCCTGATGATGACTGTAGATT 540  
DB 493 TATCTTCAGAGTGTGAGACCAACATTCGAACCTTCCTGATGATGACTGTAGATT 552  
OY 541 TGGGGCCCGATGATGAGTGTGATTTCTTCACCTTCACATGATGAAACATGAGAGTGT 600  
DB 553 TGGGGCCCGATGATGAGTGTGATTTCTTCACCTTCACATGATGAAACATGAGAGTGT 612  
OY 601 TGAGGAAGTGTATGCTACCTTATGACACAAATGGCAACACAGTCTTCAGATGTACAGCTA 660  
DB 613 TGAGGAAGTGTATGCTACCTTATGACACAAATGGCAACACAGTCTTCAGATGTACAGCTA 672  
OY 661 TGAATGGAAGGCAATGACATGATCCAGCAATGATGCTGTGAGAGTGAAGCCAAAG 720  
DB 673 TGAATGGAAGGCAATGACATGATCCAGCAATGATGCTGTGAGAGTGAAGCCAAAG 731  
OY 721 GGATGAGGTTTGGCTGCGAATGCGCATGCGCTCTCCATGGGGAGCAACCAAGCTTCT 780  
DB 722 GGATGAGGTTTGGCTGCGAATGCGCATGCGCTCTCCATGGGGAGCAACCAAGCTTCT 790  
OY 781 CACCTTTCAGAGATTCCTGC 800  
DB 791 CACCTTTCAGAGATTCCTGC 810  
RESULT 11  
ID ABR35591 standard; DNA; 741 BP.  
XX ABR35591;  
AC 08-MAY-2002 (first entry)  
DT  
XX  
DE Gene encoding novel human secreted or membrane-associated protein #10.  
XX  
KW Human; secreted protein; membrane-associated protein; hypertension;  
KW inflammatory disorder; neurological disorder; haematopoietic disorder;  
KW skeletal developmental disorder; growth abnormality; autoimmune disorder;  
KW neurodegenerative disorder; nervous system disorder; bacterial infection;  
KW peripheral myelinopathy; viral infection; cancer; obesity; diabetes;  
KW hypotension; sexual development disorder; blood disorder; gene; ds.  
XX  
XX Homo sapiens.  
XX  
XX MO200204600-A2.  
XX  
XX 17-JAN-2002.  
PD  
XX  
PF 12-JUL-2001; 2001WO-US21985.  
XX  
XX 12-JUL-2000; 2000US-218033P.  
PR 21-AUG-2000; 2000US-226517P.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX (SMIK ) SMITHKLINE BEECHAM PLC.  
XX (GLAXO ) GLAXO GROUP LTD.  
XX  
PI Agrawal P, Cogswell JP, Lai Y, Martensen SA, Rizvi SK, Strum JC;  
XX Smith RF, Xiang Z, Xie Q;  
XX WPI; 2002-188468/24.  
XX P-PSDB: AAV84371.  
XX

PT Novel secreted and membrane-associated polypeptides and polynucleotides  
PT encoding the polypeptides, for preventing, treating and ameliorating  
PT cancers, mental or sexual developmental disorders, and malignant tumours  
PT  
XX  
PS Claim 2: Page 106; 151pp; English.  
XX  
CC The present invention relates to the isolation of novel human secreted  
CC or membrane-associated proteins and the genes encoding them. The  
CC sequences of the invention are useful for treating, preventing and  
CC ameliorating various diseases such as inflammatory disorders (e.g.  
CC asthma), neurological disorders (e.g. dementia), hematopoietic  
CC disorders, skeletal developmental disorders, growth abnormalities,  
CC neurodegenerative disorders (e.g. Huntington's disease), nervous system  
CC disorders, autoimmune disorders (e.g. rheumatoid arthritis),  
CC peripheral myelinopathies, viral and bacterial infections,  
CC alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and  
CC hypotension, obesity, bulimia, anorexia, manic depression, delirium,  
CC mental retardation, Tourette's syndrome, schizophrenia, growth, mental  
CC or sexual development disorders, and dysfunction of the blood cascade  
CC system including those leading to stroke. ABK3582-ABK35609 represent  
CC the genes encoding the novel human secreted or membrane-associated  
CC proteins of the invention.  
XX  
SQ Sequence 741 BP; 191 A; 178 C; 200 G; 172 T; 0 other;

Query Match 43.3%; Score 741; DB 24; Length 741;

Best Local Similarity 100.0%; Pred. No. 3.7e-205; Mismatches 0; Gaps 0;

Matches 741: Conservative 0; Indels 0;

QY 77 ATGCTTTGAGGAGCGCTCATCTATTGGCAACTGCTGCTTTGTTTCTCTCTCTTTGCG 136  
DB 1 ATGCTTTGAGGAGCGCTCATCTATTGGCAACTGCTGCTTTGTTTCTCTCTCTTTGCG 60  
QY 137 CTGTGCAAGATGATACATGAGTCTCCACAACCGGAGACTACCCCAAGCTCAGT 196  
DB 61 CTGTGCAAGATGATACATGAGTCTCCACAACCGGAGACTACCCCAAGCTCAGT 120  
QY 197 AAGTGTTCATGAGACATACAGCTTTCAGAGTACCAAGGCGCCCTGGGCGACCGGG 256  
DB 121 AAGTGTTCATGAGACATACAGCTTTCAGAGTACCAAGGCGCCCTGGGCGACCGGG 180  
QY 257 CCTCTGGGATTCACAGAAACCATGGAACATGGAACATGGAACATGGAACATGGA 316  
DB 181 CCTCTGGGATTCACAGAAACCATGGAACATGGAACATGGAACATGGAACATGGA 240  
QY 317 GAGGCCAAGGTAGAGAGGCGCAAGGTGACCTGGGCTTGAGGGCGGCGGCGAG 376  
DB 241 GAGGCCAAGGTAGAGAGGCGCAAGGTGACCTGGGCTTGAGGGCGGCGGCGAG 300  
QY 377 CATGGGCCCAAGGAGAGAGGCGCTACCGGGGATTCCACAGACTTCGATTGGATT 436  
DB 301 CATGGGCCCAAGGAGAGAGGCGCTACCGGGGATTCCACAGACTTCGATTGGATT 360  
QY 437 ATGGCTTCTCTGCAACCCACTTCAGCAATCAGAACAGTGGATTATCTTCAGCAGT 496  
DB 361 ATGGCTTCTCTGCAACCCACTTCAGCAATCAGAACAGTGGATTATCTTCAGCAGT 420  
QY 497 GATACCAACATTTGGAACCTTTGATGTCATGACTGTTGATTTGGGGCCCAAGTAT 556  
DB 421 GATACCAACATTTGGAACCTTTGATGTCATGACTGTTGATTTGGGGCCCAAGTAT 480  
QY 557 GGTGTGATTTCTTCACTTCAGCATGATGATGAGGATTTGAGGAAGTATG 616  
DB 481 GGTGTGATTTCTTCACTTCAGCATGATGATGAGGATTTGAGGAAGTATG 540  
QY 617 TACCTTATGCAATGAGCAACAGTCTTCAGCATGATGATGAGGATTTGAGGAAG 676  
DB 541 TACCTTATGCAATGAGCAACAGTCTTCAGCATGATGATGAGGATTTGAGGAAG 600  
QY 677 TCAGATATACATCCAGCATGATGATGATGATGATGATGATGATGATGATGATG 736  
DB 601 TCAGATATACATCCAGCATGATGATGATGATGATGATGATGATGATGATGATG 660

QY 737 CGAATGGGCAATGAGCGCTCTCCATGCGGACCAACAGCTTCTCCACCTTTGAGATTC 796  
DB 661 CGAATGGGCAATGAGCGCTCTCCATGCGGACCAACAGCTTCTCCACCTTTGAGATTC 720  
QY 797 CTGCTCTTGAACACTAGTAA 817  
DB 721 CTGCTCTTGAACACTAGTAA 741

## RESULT 12

AAC9776  
ID AAC9776 standard; cDNA; 1035 BP.

XX AAC9776;

DT 08-MAR-2001 (first entry)

DE Skin cell cDNA, SEQ ID NO: 424.

XX Rat; skin cell; cytosolic; anti-inflammatory; anti-HIV;

KW neotropic; neuroprotective; vulnery; immunomodulatory; vaccine;

KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;

XX Inflammation; neurological disease; ss.

OS Ratus sp.

PN MO200069884-A2.

XX 15-MAY-2000; 2000MO-N200075.

XX 14-MAY-1999; 99US-0312283.

PA (GENE-) GENESIS RES & DEV CORP LTD.

PI Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;

DR MPI: 2001-007495/01.

XX P-PSDB; AAB55908.

PT New isolated polynucleotide used in the identification of genetic

PS disease, cancer and neurological diseases -

XX Claim 1: Page 317-318; 352pp; English.

XX The present polynucleotide encodes a polypeptide which is expressed in

CC mammalian skin cells. The polypeptide is useful for stimulating

CC keratinocyte growth and motility, inhibiting the growth of cancer cells,

CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of

CC tumours, modulating skin inflammation, stimulating the growth of

CC epithelial cells, inhibiting the binding of human immunodeficiency virus

CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and

CC neurological diseases. The polynucleotide can be used as a marker, in

CC the identification of genetic disorders, and for the design of

XX oligonucleotides for examining expression patterns.

SQ Sequence 1035 BP; 255 A; 242 C; 298 G; 240 T; 0 other;

Query Match 40.7%; Score 696.2; DB 22; Length 1035;

Best Local Similarity 82.8%; Pred. No. 5.1e-192; Mismatches 189; Conservative 0; Indels 2; Gaps 2;

QY 33 CTGCTGCTCTTCTTCAGGAGACTCTGAGCTGTTGAGATATGCTTTGAGGAGC 92  
DB 48 CCGATCAGCTTCCCGGAGAGATCTCGGATTTGTCAGAGCATGCTCAGGAGCAGC 107  
QY 93 TCATCTATGGAACAGCTGCTGCTTTGTTTCCCTCCCTTTGCTGCTGCTGCTGCTGCTG 152  
DB 108 TCGTGTGTGACACCTGCTGCTTTGCTTTCTCTCCCTTTGCTGCTGCTGCTGCTGCTG 167







Db 468 CTCACCTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTGAGCAACAATTGGAA 527  
 QY 513 ACTCTTTGATGTCATGCTGTAGATTTGGGGCCCAATACAGTACAGTATTTCTTCA 572  
 Db 528 ACTCTTTGATGTCATGCTGTAGATTTGGGGCCCAATACAGTACAGTATTTCTTCA 587  
 QY 573 CTTTCAGCATGATGATGAGATGAGATGTTGAGGAAGTATGTATGCTTATATGCAATG 632  
 Db 588 CTTTCAGCATGATGATGAGATGAGATGTTGAGGAAGTATGTATGCTTATATGCAATG 647  
 QY 633 GCACACAGTCTTTCAGCATGATGAGATGTTGAGGAAGTATGTATGCTTATATGCAATG 692  
 Db 648 GTAACACGCTGTTCAGCATGATGAGATGTTGAGGAAGTATGTATGCTTATATGCAATG 707  
 QY 693 ATCATGCTGTGTGAGTGAAGTGAAGCAAGGATGAGTGTGCTGAGTGGCAATGGCG 752  
 Db 708 ACCATGCAAGTGTGAAGTGTGAGTGAAGCAAGGATGAGTGTGCTGAGTGGCAATGGCG 767  
 QY 753 CTCTCATGAGGAGCACCACCAAGCTTCTCCAGCTTTCAGAGATTCCTGCTTTTGAAGTA 812  
 Db 768 CCTTCATGAGGAGCACCACCAAGCTTCTCCAGCTTTCAGAGATTCCTGCTTTTGAAGTA 827  
 QY 813 ACTAATATATGACTAGATAGCTTCCACTTGGGGAAGACTTGTAGCTGAGCT-GATTGG 871  
 Db 828 AGTATGAGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 887  
 QY 872 TTACATCTGAGGACATTTAAAGTGTGAGGTTTACATTTGCTGATTCATAAATTAATG 931  
 Db 888 TTAGATCTGAGGAGTGTGAGGTTTACATTTGCTGATTCATAAATTAATG 946  
 QY 932 GTTCAGATGTTGCTGAGGTTTACATTTGCTGATTCATAAATTAATG 991  
 Db 947 GTTCAGATGTTGCTGAGGTTTACATTTGCTGATTCATAAATTAATG 1006  
 QY 992 AGAATCAACCAAAATAGCTTCTCAGA 1020  
 Db 1007 AGAATCAACCAAAATAGCTTCTCAGA 1035

RESULT 14  
 AA261633  
 ID AA261633 standard: cDNA: 1123 BP.  
 AC AA261633;  
 XX  
 DT 27-MAR-2000 (first entry)  
 DE cDNA encoding rat skin cell secreted protein, SEQ ID NO:28.  
 XX  
 KW Skin: dermal papilla; keratinocyte; neonatal foreskin fibroblast;  
 KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell;  
 KW secreted; transmembrane; inflammation; cancer; neurological disease;  
 KW angiogenesis; tumour vascularisation; growth disorder;  
 KW developmental disorder; skin wound; hair follicle disorder;  
 KW anti-inflammatory; cytostatic; neuroprotective; vulnery; ss.  
 OS Rattus sp.  
 XX  
 PN W09955865-A1.  
 PD 04-NOV-1999.  
 XX  
 PE 29-APR-1999; 99WO-NZ00051.  
 PR 29-APR-1998; 98US-0069726.  
 PR 09-NOV-1998; 98US-0188930.  
 XX  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 XX  
 PI Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;  
 XX  
 DR WPI, 2000-072177/06.  
 XX

PT Novel polynucleotides useful for the treatment of various conditions  
 PT including wounds and cancer  
 XX  
 PS Claim 1: Page 73: 235pp: English.  
 XX  
 CC The invention relates to novel nucleic acid sequences derived from rat  
 CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,  
 CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying  
 CC cells. Polypeptides of the invention may be used to treat inflammation,  
 CC cancer and neurological diseases. The proteins may be used to stimulate  
 CC the growth and motility of keratinocytes, to inhibit the growth of  
 CC cancer cells, to modulate angiogenesis and tumour vascularisation, to  
 CC inhibit skin inflammation, to modulate epithelial cell growth and to  
 CC inhibit binding of HIV-1 to leukocytes. The invention may also be used  
 CC to treat growth and developmental defects, skin wounds and hair follicle  
 CC disorders. Sequences AA261606-261832 represent cDNA sequences derived  
 CC from several mouse, rat or human skin cell types. Sequences  
 CC AA261606-261649, AA261725-261765, AA261802-261811 and AA261826 encode  
 CC proteins with an N-terminal signal sequence, indicating that the proteins  
 CC are secreted. Sequences AA261650-261668, AA261766-261780, AA261812-261817  
 CC and AA261827-261829 encode proteins with one or more putative  
 CC transmembrane domains.  
 XX  
 SQ Sequence 1123 BP: 277 A: 266 C: 321 G: 258 T: 1 other:  
 Query Match 40.7%; Score 696.2; DB 21; Length 1123;  
 Best Local Similarity 82.8%; Pred. No. 5.3e-192;  
 Matches 819; Conservative 0; Mismatches 168; Indels 2; Gaps 2;

QY 33 CTCTGCTGCTTCTCAGGAGACTGTGAGCTCTGTTGAAATCATCTTTGGAGGCAG 92  
 Db 136 CCCATCAGCTTCCCGGGAGATGCTGCGATTTGACAGGACATGTCAGAGGCAGC 195  
 QY 93 TCATCTATGCGAATGCTGCTGCTTTTCTCCCTTTTGGCTGCTGCTGCTGCTGCTGCT 152  
 Db 196 TCGTGTGGGAGCTGCTGCTGCTTCTTCTCCATTTGCTGCTGCTGCTGCTGCTGCTGCT 255  
 QY 153 ACATGAGCTCTCACAACCGGAGAGCTACCCAGAGCTGAGTGAAGTGTGATGAG 212  
 Db 256 ACATGAGCTCTCACAACCGGAGAGCTACCCAGAGCTGAGTGAAGTGTGATGAG 315  
 QY 213 ACTACAGCTTTCAGGCTACCAAGGCCCCCTGAGGCCACCGGCCCCCTGAGCTTCAG 272  
 Db 316 ATTATGATTTCCGTGTTACCAAGGCCCCCTGAGGCCACCGGCCCCCTGAGCTTCAG 375  
 QY 273 GAACCATGGAACCAATGGCAACATGGAGCCAGCTGATGAGGAGCAAAAGTGAG 332  
 Db 376 GAACCATGGAACCAATGGCAACATGGAGCCAGCTGATGAGGAGCAAAAGTGAG 435  
 QY 333 AGGCGACAAAGGTGACCTGAGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 392  
 Db 436 AAGGACACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 495  
 QY 393 AGAAGGCTACCGGGGATTCACACGAACTTCAATGATTCATGCTGCTGAGCA 452  
 Db 496 AGAAGGATACCGGGGATTCACACGAGAGCTGAGTTCATGCTGCTGAGCA 555  
 QY 453 CCCACTTCAGCAATGAGACAGGAGGATTCATGCTGAGAGTGTGAGCAACATGGAA 512  
 Db 556 CTCACCTTCAGCAATGAGACAGGAGGATTCATGCTGAGAGTGTGAGCAACATGGAA 615  
 QY 513 ACTCTTTGATGTCATGCTGTAGATTTGGGGCCCAATACAGTACAGTATTTCTTCA 572  
 Db 616 ACTCTTTGATGTCATGCTGTAGATTTGGGGCCCAATACAGTACAGTATTTCTTCA 675  
 QY 573 CTTTCAGCATGATGATGAGATGAGATGTTGAGGAAGTATGTATGCTTATATGCAATG 632  
 Db 676 CTTTCAGCATGATGATGAGATGAGATGTTGAGGAAGTATGTATGCTTATATGCAATG 735  
 QY 633 GCACACAGTCTTTCAGCATGATGAGATGTTGAGGAAGTATGTATGCTTATATGCAATG 692  
 Db 736 GTAACACGCTGTTCAGCATGATGAGATGTTGAGGAAGTATGTATGCTTATATGCAATG 795



Db 976 TTAGCATCTGAGGGGTGTGAGFTG-GCCTCTCTATGAGTATTTAACTGTTACATTG 1034  
QY 932 GTTGCATGTGTTGTCAGCTACAGTACACCAATATATGTGACATTCAGGGGCTCAGA 991  
Db 1035 GTCACACTGCTACTCTAATCTAATGACATACCAATTAATGTAATCTTAGGGGCTAGGA 1094  
QY 992 AGATCAACCAACAAATATAGTCTTCTCAGA 1020  
Db 1095 AGATAGACCAACAGTAAATATTCACAGA 1123

Search completed: January 15, 2003, 17:41:35  
Job time : 362 secs



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PRIOR FILING DATE: 1999-03-24  
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PRIOR FILING DATE: 1999-03-31  
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PRIOR FILING DATE: 1999-04-05  
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PRIOR APPLICATION NUMBER: PCT/US01/21066  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 80  
SEQ ID NO 1  
LENGTH: 1712  
TYPE: DNA  
ORGANISM: Homo Saplen  
us-10-036-041-1

Query Match 100.0%; Score 1712; DB 9; Length 1712;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1712; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGCATCTGCCGAGAGACACGCTCTGAGACTCTGCTCTTCTGAGGAGACTCTGA 60  
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Db 61 GGCCTGTGGAGAACATGCTTTGGAGGACATCTATTGCACTGCTGCTTTGTT 120  
QY 121 TTTCCTCCCTTTTGGCTGTCAAGATGATACATGAGCTCCACAAACCGAGACT 180  
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Db 121 TTTCCTCCCTTTTGGCTGTCAAGATGATACATGAGCTCCACAAACCGAGACT 180  
QY 181 ACCCCAGACTGACATGATGTTGTCAATGAGACTACAGCTTTGAGGCTACCAAGGCC 240  
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Db 181 ACCCCAGACTGACATGATGTTGTCAATGAGACTACAGCTTTGAGGCTACCAAGGCC 240  
QY 241 CCTGGGCCACCGGCCCTCTCTGCAATTCAGAAACCATGGAACAATGGCAATGG 300  
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Db 241 CCTGGGCCACCGGCCCTCTCTGCAATTCAGAAACCATGGAACAATGGCAATGG 300  
QY 301 AGCCACGTGTCATGAAGAGCCAAAGTGAGAGGGGCAAAAGTACCTGGGGCCTCG 360  
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Db 301 AGCCACGTGTCATGAAGAGCCAAAGTGAGAGGGGCAAAAGTACCTGGGGCCTCG 360  
QY 361 AGGGAGCGGGGCGCAGCATGGCCCCCAAGAGAGAGGGCTACCCGGGATTTCCACCA 420  
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Db 361 AGGGAGCGGGGCGCAGCATGGCCCCCAAGAGAGAGGGCTACCCGGGATTTCCACCA 420  
QY 421 ACTTCAGATTCATTCATGCTTCTGCAACCCACTTCAGCAATCAGAAAGTGGAT 480  
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Db 421 ACTTCAGATTCATTCATGCTTCTGCAACCCACTTCAGCAATCAGAAAGTGGAT 480  
QY 481 TATCTCAGAGCTGTAGAGCAACATTTGGAACCTCTTGTATGATCATGATGGAGATT 540  
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QY 541 TGGGGCCCCAGTATCAGGTGTATTTCTTCACTTCAGATGATGAGAGATGT 600  
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Db 661 TGAATGAAGGCAAAATCAGATACATCCAGCAATCATGCTGTGTAAGCTAGGCAAAAG 720  
QY 721 GGATGAGTTTGGCTGGCAATGGCAATGGGCTCTCCATGGGAGCAACCAAGCTTCTC 780  
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Db 721 GGATGAGTTTGGCTGGCAATGGGCAATGGGCTCTCCATGGGAGCAACCAAGCTTCTC 780

QY 781 CACCTTGCAGAGTTCCTGCTCTTTGAACTAGTAATATATAGTACATAGTCCAC 840  
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DB 781 CACCTTGCAGAGTTCCTGCTCTTTGAACTAGTAATATATAGTACATAGTCCAC 840  
QY 841 TTTGGGGAAGACTTGTAGCTGAGCTGATTTGTAGCATCTGAGCAATTAAGTTGAG 900  
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DB 841 TTTGGGGAAGACTTGTAGCTGAGCTGATTTGTAGCATCTGAGCAATTAAGTTGAG 900  
QY 901 GTTTACATGCTGATTAATTAATTTGTTGCAATGTTTGCACCTACAGTACA 960  
|||||  
DB 901 GTTTACATGCTGATTAATTAATTTGTTGCAATGTTTGCACCTACAGTACA 960  
QY 961 CCAATATGTTGACAAATTCAGGGGCTCAGAAATCAACCAAAATAGTCTTCAGA 1020  
|||||  
DB 961 CCAATATGTTGACAAATTCAGGGGCTCAGAAATCAACCAAAATAGTCTTCAGA 1020  
QY 1021 TGAACCTGACATATATCTGACAGCTCTTATCCTCTTCTGACCTTAAGATTAAT 1080  
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DB 1021 TGAACCTGACATATATCTGACAGCTCTTATCCTCTTCTGACCTTAAGATTAAT 1080  
QY 1081 TCTGCTGACAGCTGAGTGAATATTTTCTATCAGAGAGTCTATTCGAAAGATTT 1140  
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DB 1081 TCTGCTGACAGCTGAGTGAATATTTTCTATCAGAGAGTCTATTCGAAAGATTT 1140  
QY 1141 TTGACTACTCTGCTTTTATTAATACAGTTTTCAGAAACCCCTGAAGTTTAAGTTCA 1200  
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DB 1141 TTGACTACTCTGCTTTTATTAATTAATACAGTTTTCAGAAACCCCTGAAGTTTAAGTTCA 1200  
QY 1201 TTAATCTTTATTAATATTTGAGAAATCGAGTATGATATGACAGAGGCTGGGCAAGAA 1260  
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DB 1201 TTAATCTTTATTAATATTTGAGAAATCGAGTATGATATGACAGAGGCTGGGCAAGAA 1260  
QY 1261 CAGGGGCACTACTGCTCTTATTAATTAATTTAGTCCCTGCTGCTGCTGCTGCTGCTG 1320  
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DB 1261 CAGGGGCACTACTGCTCTTATTAATTAATTTAGTCCCTGCTGCTGCTGCTGCTGCTG 1320  
QY 1321 ACCCTTCTTGTGATCCCAAAATACATTAATAACTGTAATTCACATGCTATTTT 1380  
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DB 1321 ACCCTTCTTGTGATCCCAAAATACATTAATAACTGTAATTCACATGCTATTTT 1380  
QY 1381 TAAAGTCAATATATTTAGCTATTAAGTCTGACAGTAAATGCTGTTGTTGTTGTTGTT 1440  
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DB 1381 TAAAGTCAATATATTTAGCTATTAAGTCTGACAGTAAATGCTGTTGTTGTTGTTGTT 1440  
QY 1441 ATGTTCCCGCATGCGCCCAACTCGAGTGTGGGCTGAGAGGTTGAGGTTGCTATTT 1500  
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DB 1441 ATGTTCCCGCATGCGCCCAACTCGAGTGTGGGCTGAGAGGTTGAGGTTGCTATTT 1500  
QY 1501 AACCAATGTCATTAATATCTCATAGAGTACAGTCCCAATAGATTTCAATGTTGCATG 1560  
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DB 1501 AACCAATGTCATTAATATCTCATAGAGTACAGTCCCAATAGATTTCAATGTTGCATG 1560  
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DB 1561 TTGACCAAGGAGATTTATATCTGAAGAATACATATTAATTAATTAATTAATTAATTA 1620  
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DB 1621 ATTTGCACTGCTTATTAATTAATCTGCAAGAAATGTAATGCAATATATGAA 1680  
QY 1681 ATTAACACACCTTTGTTAAAGATTAATAAAAAA 1712  
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DB 1681 ATTAACACACCTTTGTTAAAGATTAATAAAAAA 1712

RESULT 2  
US-10-035-855-1  
: Sequence 1, Application US/10035855  
: Publication No. US20030008348A1  
: GENERAL INFORMATION:  
: APPLICANT: Desnoyers, Luc  
: APPLICANT: Eaton, Dan L.

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Guirney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: ZHANG, ZEMIN  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3030R1C4  
CURRENT APPLICATION NUMBER: US/10/035, 855  
CURRENT FILING DATE: 2001-12-26  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/112514  
PRIOR FILING DATE: 1998-12-15  
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PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 80  
SEQ ID NO 1  
LENGTH: 1712  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-035-855-1

Query Match 100.0%; Score 1712; DB 9; Length 1712;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1712; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 361 AGGGAGCGGGGGGAGCACTGGCCCCAAAGAGAGAGAGGGCTACCCGGGATTTCCACCA 420  
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DB 421 ACTTCAGATTGATTCATGAGCTTCTCTGCGAACCCACTTCAGCATGCAAGAGTGGAT 480  
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DB 481 TATCTTACAGAGTGTGAGCAACCAATTTGAAACTCTTTGATGTCAATGAGTGTAGATT 540  
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DB 601 TGAGGAAGTGTATGTATCTTATGCAACATGCGACAGCTTCACATGATACGCTA 660  
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DB 661 TGAATGAAGGCAAAATCAGATACATCCAGCAATCATCTGTGTAAGTACGCAAAAG 720  
QY 721 GGATGAGTGTGGCTGCGCAATGGGCAATGGGCTTCATGGGACCAACGCTTCTC 780  
DB 721 GGATGAGTGTGGCTGCGCAATGGGCAATGGGCTTCATGGGACCAACGCTTCTC 780  
QY 781 CACCTTGCAGAGATTCCGCTCTTGAAGCTAAGTAATATGACTGATAGCTCCAC 840  
DB 781 CACCTTGCAGAGATTCCGCTCTTGAAGCTAAGTAATATGACTGATAGCTCCAC 840  
QY 841 TTTGGGGAAGCTGTAGCTGAGCTGATTTGTACGATCTGAGAACTTAAAGTTGAGG 900  
DB 841 TTTGGGGAAGCTGTAGCTGAGCTGATTTGTACGATCTGAGAACTTAAAGTTGAGG 900  
QY 901 GTTTTACATTCCTGTATTTCAAAAATTTATGTTGCAATGTTTTCACGCTACAGTGTACA 960  
DB 901 GTTTTACATTCCTGTATTTCAAAAATTTATGTTGCAATGTTTTCACGCTACAGTGTACA 960  
QY 961 CCATTAATGTGGAACAATTCAGGGGCTCAGAAAGATCAACCAAAATAGTCTTCAGA 1020  
DB 961 CCATTAATGTGGAACAATTCAGGGGCTCAGAAAGATCAACCAAAATAGTCTTCAGA 1020  
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DB 1021 TGACCTTGACTAATATACATCTTTATACATCTTTCTTGGCACCCTAAAGATAT 1080  
QY 1081 TCTCTCTGAGGAGAGGTGGAATATTTTCTTATCACAAGATCATTTGCAAGATTT 1140  
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QY 1141 TTGACTACTGCTTTTATTTAATACAGTTTTCAGAGACCCCTGAGTTTTAAGTTCA 1200  
DB 1141 TTGACTACTGCTTTTATTTAATTTAATACAGTTTTCAGAGACCCCTGAGTTTTAAGTTCA 1200  
QY 1201 TTATTTCTTATTAACATTTGAAGAAATCGATGTATGATGACAGGCTGGGCAAGAA 1260  
DB 1201 TTATTTCTTATTAACATTTGAAGAAATCGATGTATGATGACAGGCTGGGCAAGAA 1260  
QY 1261 CAGGGGCACTAGCTGCTTATTAAGTAAATTTAGTCCCTCGGTGTCAGCTTACGCTTTG 1320  
DB 1261 CAGGGGCACTAGCTGCTTATTAAGTAAATTTAGTCCCTCGGTGTCAGCTTACGCTTTG 1320  
QY 1321 ACCCTTCTTTTGTATCCAAAATATACATTTAAACTGTGAATTCACATATCAATGCTATT 1380



Db 1321 ACCCTTCCTTTGATCCACAAATATCAATTAACCTGATTCACATCAATGCTATTT 1380  
Qy 1381 TAAAGTCAATAGATTTTACCTATTAAGTCTTGACCAAGTAAGTGTGTTGTTGTTG 1440  
Db 1381 TAAAGTCAATAGATTTTACCTATTAAGTCTTGACCAAGTAAGTGTGTTGTTGTTG 1440  
Qy 1441 AAGTCCCCACATGCCCCCAACTCGGATGCGGGGTAGAGGTTGAGGTTGACTATT 1500  
Db 1441 AAGTCCCCACATGCCCCCAACTCGGATGCGGGGTAGAGGTTGAGGTTGACTATT 1500  
Qy 1501 AACAAATGTCATTAATATCTCATAGAGTACACTGCCAATAGATTAATGTTCCATG 1560  
Db 1501 AACAAATGTCATTAATATCTCATAGAGTACACTGCCAATAGATTAATGTTCCATG 1560  
Qy 1561 TTGACCAAGAGGATTTTATATCTGAAGACATCACTATTAATTAATACCTTGAGAAAG 1620  
Db 1561 TTGACCAAGAGGATTTTATATCTGAAGACATCACTATTAATTAATACCTTGAGAAAG 1620  
Qy 1621 ATTTTGACCTGCTTAAGTAAAGTGTGCGAAGAAATGTATGACATATATGGA 1680  
Db 1621 ATTTTGACCTGCTTAAGTAAAGTGTGCGAAGAAATGTATGACATATATGGA 1680  
Qy 1681 ATAAACACACCTTTGTTAAAGATTAATAAAAAA 1712  
Db 1681 ATAAACACACCTTTGTTAAAGATTAATAAAAAA 1712

RESULT 3  
US-10-036-342-1  
Sequence 1, Application US/10036342  
Patent No. US20020090681A1  
GENERAL INFORMATION:  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Watanabe, Collin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhaog, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3030R1CS  
CURRENT APPLICATION NUMBER: US/10/036,342  
PRIOR FILING DATE: 2001-12-26  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/112514  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/113300  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113430  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/113605  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/114140  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/115552  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/116843  
PRIOR FILING DATE: 1999-01-22  
PRIOR APPLICATION NUMBER: 60/125774  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 60/125778  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 60/125826  
PRIOR FILING DATE: 1999-03-24  
PRIOR APPLICATION NUMBER: 60/127035

PRIOR FILING DATE: 1999-03-31  
PRIOR APPLICATION NUMBER: 60/127706  
PRIOR FILING DATE: 1999-04-05  
PRIOR APPLICATION NUMBER: 60/129122  
PRIOR FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: 60/130359  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: 60/131270  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/131272  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/131291  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/132371  
PRIOR FILING DATE: 1999-05-04  
PRIOR APPLICATION NUMBER: 60/132379  
PRIOR FILING DATE: 1999-05-04  
PRIOR APPLICATION NUMBER: 60/132383  
PRIOR FILING DATE: 1999-05-04  
PRIOR APPLICATION NUMBER: 60/135750  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: 60/138166  
PRIOR FILING DATE: 1999-06-08  
PRIOR APPLICATION NUMBER: 60/144791  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/146970  
PRIOR FILING DATE: 1999-08-03  
PRIOR APPLICATION NUMBER: 60/162506  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: 09/311832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 09/380142  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/644848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 09/747259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 09/816744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: 09/854208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/854280  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/874503  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: 09/869599  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: 09/908,827  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: PCT/US99/10733  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: PCT/US99/28551  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30720  
PRIOR FILING DATE: 1999-12-22  
PRIOR APPLICATION NUMBER: PCT/US00/05601  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: PCT/US00/14042  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: PCT/US00/23522  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28

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; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 1
; LENGTH: 1712
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-036-342-1

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Query Match      100.0%; Score 1712; DB 12; Length 1712;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1712; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GGCATCTGCCGAGAGACCAAGCTCTGGAGCTGTGCTCTTCTCAGGGAGACTGTA 60
Db 1 GGCATCTGCCGAGAGACCAAGCTCTGGAGCTGTGCTCTTCTCAGGGAGACTGTA 60
OY 61 GGCCTGTGAGATCATGCTTTGGAGGCAAGCTCATCTATTGGCACTGCTGGCTTGT 120
Db 61 GGCCTGTGAGATCATGCTTTGGAGGCAAGCTCATCTATTGGCACTGCTGGCTTGT 120
OY 121 TTTTCCTCCCTTTTGGCTGTGTCAAGATGATACATGAGAGCTCTCCACAAACCGAGACT 180
Db 121 TTTTCCTCCCTTTTGGCTGTGTCAAGATGATACATGAGAGCTCTCCACAAACCGAGACT 180
OY 181 ACCCCAGACTGAGTAAGTGTGTCAAGAGACTATGAGAGCTTTGAGGCTTACCAAGGCC 240
Db 181 ACCCCAGACTGAGTAAGTGTGTCAAGAGACTATGAGAGCTTTGAGGCTTACCAAGGCC 240
OY 241 CCTTGGGCCACCGGGCCCTCTGGCATTCAGGAACCATGGAACCAATGGCAACATGG 300
Db 241 CCTTGGGCCACCGGGCCCTCTGGCATTCAGGAACCATGGAACCAATGGCAACATGG 300
OY 301 AGCCACAGTGTGAAGAGCAAGAGTGAAGAGGAGGCAAGAGTGAAGTGGGGCCCTCG 360
Db 301 AGCCACAGTGTGAAGAGCAAGAGTGAAGAGGAGGCAAGAGTGAAGTGGGGCCCTCG 360
OY 361 AGGGGAGCGGGGCGAGATGGCCCAAGAGAGAGAGGAGGCTACCCGGGAGTTCCACAGA 420
Db 361 AGGGGAGCGGGGCGAGATGGCCCAAGAGAGAGAGGAGGCTACCCGGGAGTTCCACAGA 420
OY 421 ACTTCAGATTGATTCATGAGCTTCTGCGCAACCCACTTCAGCAATGAGAACAGTGGGAT 480
Db 421 ACTTCAGATTGATTCATGAGCTTCTGCGCAACCCACTTCAGCAATGAGAACAGTGGGAT 480
OY 481 TATCTTCAGAGAGTGTGAAGCAACATTTGGAATCTTTGATGTGATGACTGTAAGTT 540
Db 481 TATCTTCAGAGAGTGTGAAGCAACATTTGGAATCTTTGATGTGATGACTGTAAGTT 540
OY 541 TGGGGCCCCAGTATCAGGTGTGATTTCTTCACCTTCAGCATGATGAGAGATGT 600
Db 541 TGGGGCCCCAGTATCAGGTGTGATTTCTTCACCTTCAGCATGATGAGAGATGT 600
OY 601 TGAAGAGTGTATGTGATCTTATGACAAATGGCAACAGTCTTCAGCATGATGAGAGT 660
Db 601 TGAAGAGTGTATGTGATCTTATGACAAATGGCAACAGTCTTCAGCATGATGAGAGT 660
OY 661 TGAATGAAGGGAATACATATACATACCAATCATGCTGTGTGAAGTGAAGCAAGG 720
Db 661 TGAATGAAGGGAATACATATACATACCAATCATGCTGTGTGAAGTGAAGCAAGG 720
OY 721 GGATGAAGTGTGCTGGGAATGGGCAATGGGCTCTCCATGGGAGCAACCAACCTTCTC 780
Db 721 GGATGAAGTGTGCTGGGAATGGGCAATGGGCTCTCCATGGGAGCAACCAACCTTCTC 780
OY 781 CACCTTTCAGAGATCTCTGCTTTTGAAGTAAGTAATATATGACTAGAAATAGCTCCAC 840
Db 781 CACCTTTCAGAGATCTCTGCTTTTGAAGTAAGTAATATATGACTAGAAATAGCTCCAC 840

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Db 781 CACCTTTCAGAGATCTCTGCTTTTGAAGTAAGTAATATATGACTAGAAATAGCTCCAC 840
OY 841 TTTGGGAGAGACTGTAGCTGAGCTGATTTGTATGATCTGTGAGCAACATTAAGTTGAGG 900
Db 841 TTTGGGAGAGACTGTAGCTGAGCTGATTTGTATGATCTGTGAGCAACATTAAGTTGAGG 900
OY 901 GTTTTACATTCCTGTATTCAAAATAATTAATGTTGCAATGTTGTTACAGCTACAGGTACA 960
Db 901 GTTTTACATTCCTGTATTCAAAATAATTAATGTTGCAATGTTGTTACAGCTACAGGTACA 960
OY 961 CCAATTAATGTTGAGCAATTCAGGGGCTCAGAGAAATCAACCAAAATAATGCTTCTCAGA 1020
Db 961 CCAATTAATGTTGAGCAATTCAGGGGCTCAGAGAAATCAACCAAAATAATGCTTCTCAGA 1020
OY 1021 TGACCTGACATTAATTAATCTAGCATCTTTATCAGCTTTTCTGGCAGCTTAAAGATAT 1080
Db 1021 TGACCTGACATTAATTAATCTAGCATCTTTATCAGCTTTTCTGGCAGCTTAAAGATAT 1080
OY 1081 TCTCCTGAGCAGAGTGGAAATATTTTCTATACAGAGATCATTTGCAAGAAAT 1140
Db 1081 TCTCCTGAGCAGAGTGGAAATATTTTCTATACAGAGATCATTTGCAAGAAAT 1140
OY 1141 TTGACTACTGCTTTTAATTAATTAATCCAGTTTTCAGGAAACCCCTGAAGTTTAAGTCA 1200
Db 1141 TTGACTACTGCTTTTAATTAATTAATCCAGTTTTCAGGAAACCCCTGAAGTTTAAGTCA 1200
OY 1201 TTAATCTTTAATTAATTAATGAAGAAATGAGATGTATGATATGACAGGGCTGGGCAAG 1260
Db 1201 TTAATCTTTAATTAATTAATGAAGAAATGAGATGTATGATATGACAGGGCTGGGCAAG 1260
OY 1261 CAGGGGCACTGCTGCTTTAATTAATTAATAGTCCCTCCGCTGTTAGCTTACCTTTG 1320
Db 1261 CAGGGGCACTGCTGCTTTAATTAATTAATAGTCCCTCCGCTGTTAGCTTACCTTTG 1320
OY 1321 ACCCTTCTCTTTGATCCACAAATTAATTAATTAATCTGAAATTCACATACATGCTAAT 1380
Db 1321 ACCCTTCTCTTTGATCCACAAATTAATTAATTAATCTGAAATTCACATACATGCTAAT 1380
OY 1381 TAAAGTCAATGATTTTATGCTATTAAGTGTGTTGACACATTAATGTTGTATTTTGT 1440
Db 1381 TAAAGTCAATGATTTTATGCTATTAAGTGTGTTGACACATTAATGTTGTATTTTGT 1440
OY 1441 ATGTCCCCCATGCGCCCAACTGCGATGTGGGCTCAGAGAGTTGAGGTTGCTACTATT 1500
Db 1441 ATGTCCCCCATGCGCCCAACTGCGATGTGGGCTCAGAGAGTTGAGGTTGCTACTATT 1500
OY 1501 AACAAATGCTAATAATCTCATAGAGGTACAGTCCCAATAGATATTCAAATGTTGCATG 1560
Db 1501 AACAAATGCTAATAATCTCATAGAGGTACAGTCCCAATAGATATTCAAATGTTGCATG 1560
OY 1561 TTGACACAGAGGATTTTATATCTGAAGACATTAATTAATTAATACCTTAGAGAAAG 1620
Db 1561 TTGACACAGAGGATTTTATATCTGAAGACATTAATTAATTAATACCTTAGAGAAAG 1620
OY 1621 ATTTGACCTGCTTTAGATTAATCTGAGCAAGAAATTAATGAGCAATATATGGA 1680
Db 1621 ATTTGACCTGCTTTAGATTAATCTGAGCAAGAAATTAATGAGCAATATATGGA 1680
OY 1681 ATTAACACACCTTTGTTAAAGATAAAAAAA 1712
Db 1681 ATTAACACACCTTTGTTAAAGATAAAAAAA 1712

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RESULT 4
US-09-822-849A-359
; Sequence 359, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clair, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.

```

```

: APPLICANT: Resnick, Richard J.
: APPLICANT: Gulukota, Kamalakara
: APPLICANT: Graham, James R.
: APPLICANT: Genetics Institute, Inc.
: TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
: FILE REFERENCE: GIN 6403
: CURRENT APPLICATION NUMBER: US/09/822,849A
: CURRENT FILING DATE: 2001-09-04
: PRIOR APPLICATION NUMBER: 60/195,582
: PRIOR FILING DATE: 2000-04-06
: NUMBER OF SEQ ID NOS: 598
: SOFTWARE: Patent Ver. 2.0
: SEQ ID NO 359
: LENGTH: 1608
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-822-849A-359

Query Match      79.6%  Score 1363.2:  DB 10;  Length 1608;
Best Local Similarity 99.8%:  Pred. No. 0:
Matches 1365:  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0:

QY  337  CGACAAGGTGACCTGGGCGCTCGAGGGAGCGGGGCGAGCATGGCCCAAGAGAGAA 396
DB    1  CGACAAGGTGACCTGGGCGCTCGAGGGAGCGGGGCGAGCATGGCCCAAGAGAGAA 60
QY  397  GGGCTACCCGGGGATTCGCCAGAACTTCAGATTCATTCGCTTCCTGGCAACCA 456
DB    61  GGGCTACCCGGGGATTCGCCAGAACTTCAGATTCATTCGCTTCCTGGCAACCA 120
QY  457  CTTGACCAATCAGAACAGAGGGGATTCCTTCAGCAGCTGTTGAGCAACAACTTGAACCT 516
DB   121  CTTGACCAATCAGAACAGAGGGGATTCCTTCAGCAGCTGTTGAGCAACAACTTGAACCT 180
QY  517  CTTGATGTCAGTACGTAGATTTGGGGCCCGCATATCAGGTGTATTTCTTCACCTT 576
DB   181  CTTGATGTCAGTACGTAGATTTGGGGCCCGCATATCAGGTGTATTTCTTCACCTT 240
QY  577  CAGCATGATGAAGCATGAGATTTTGAAGAGAGTATGTACCTTATGCAATGGCA 636
DB   241  CAGCATGATGAAGCATGAGATTTTGAAGAGAGTATGTATGTATGCAATGGCA 300
QY  637  CACAGTCTCAGCATATGAGTAAATGAAGGCAATCAGATACATCCAGCAATCA 696
DB   301  CACAGTCTCAGCATATGAGTAAATGAAGGCAATCAGATACATCCAGCAATCA 360
QY  697  TGGTGTGTCGAAGCTAGCCAAAGGGGATGAGTTGGCTCGAATGGCAATGGCCTCT 756
DB   361  TGGTGTGTCGAAGCTAGCCAAAGGGGATGAGTTGGCTCGAATGGCAATGGCCTCT 420
QY  757  CCATGGGAGCACCAACGCTTCTCCACCTTTGAGAGATTCCTCTTTTAAACTAGTA 816
DB   421  CCATGGGAGCACCAACGCTTCTCCACCTTTGAGAGATTCCTCTTTTAAACTAGTA 480
QY  817  AATATATGACTAGATAGCTCCACTTTGGGAGAGACTTGTAGCTGAGCTGATTTGTAG 876
DB   481  AATATATGACTAGATAGCTCCACTTTGGGAGAGACTTGTAGCTGAGCTGATTTGTAG 540
QY  877  ATCTGAGAGAACTTAAAGTTGAGGGTTTACATTTGCTGATTTCAAAAATTAATTTGCTGC 936
DB   541  ATCTGAGAGAACTTAAAGTTGAGGGTTTACATTTGCTGATTTCAAAAATTAATTTGCTGC 600
QY  937  AATGTGTTCACGCTACAGTACACCAATATTTGGACATTCAGGGGCTCGAAGAAAT 996
DB   601  AATGTGTTCACGCTACAGTACACCAATATTTGGACATTCAGGGGCTCGAAGAAAT 660
QY  997  CAACGCAAAATAGTCTTCAGATGACCTTGACTATATACTCAGCATCTTATATCCTC 1056
DB   661  CAACGCAAAATAGTCTTCAGATGACCTTGACTATATACTCAGCATCTTATATCCTC 720
QY  1057  TTTCTTGGCAGCTTAAAGATAATTTCTCTCTGACGAGGCTTGAATATTTTCTTAT 1116
DB   721  TTTCTTGGCAGCTTAAAGATAATTTCTCTCTGACGAGGCTTGAATATTTTCTTAT 780

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QY  1117  CACAGAGTCATTTGCAAGAATTTTACTACTGCTTCTTAAATTAATACAGATTTTCA 1176
DB   781  CACAGAGTCATTTGCAAGAATTTTACTACTGCTTCTTAAATTAATACAGATTTTCA 840
QY  1177  GGAACCCCTGAAGTTTAAAGTTCATTTCTTTAATACATTTGAGAGAAATCGATAGT 1236
DB   841  GGAACCCCTGAAGTTTAAAGTTCATTTCTTTAATACATTTGAGAGAAATCGATAGT 900
QY  1237  GATATGACAGGGCTGGGCAAGAACAGGGGCACTAGCTGCTTATTTAGCTATTTACTGC 1286
DB   901  GATATGACAGGGCTGGGCAAGAACAGGGGCACTAGCTGCTTATTTAGCTATTTACTGC 960
QY  1297  CCTCCGTTACAGTTCAGCTTACGCTTTCAGCCCTTCTTTGATCCAAATATCATTAAC 1356
DB   961  CCTCCGTTACAGTTCAGCTTACGCTTTCAGCCCTTCTTTGATCCAAATATCATTAAC 1020
QY  1357  CTGAATTCACATTCATTCATTTTAAAGTCAATATAGATTTTAAAGTTCATTAAGCTG 1416
DB   1021  CTGAATTCACATTCATTCATTTTAAAGTCAATATAGATTTTAAAGTTCATTAAGCTG 1080
QY  1417  AGTAATGTGTTGATTTTGTATGTTCCCCACATCGCCCACTTCGATGCG 1476
DB   1081  AGTAATGTGTTGATTTTGTATGTTCCCCACATCGCCCACTTCGATGCG 1140
QY  1477  GTCAGAGGTTGAGTTCATTTACCAATATGATTAATATCTCATAGAGATGACAGTGC 1536
DB   1141  GTCAGAGGTTGAGTTCATTTACCAATATGATTAATATCTCATAGAGATGACAGTGC 1200
QY  1537  CAATGATATTCATTAATGTTGCATGTTGACCAAGAGGATTTTATATCTGAAGAACATAC 1596
DB   1201  CAATGATATTCATTAATGTTGCATGTTGACCAAGAGGATTTTATATCTGAAGAACATAC 1260
QY  1597  TATTATTAATTAATTTAGAGAAAGATTTTACCTGCTTATGATTAATTAATCTGCAAGAA 1656
DB   1261  TATTATTAATTAATTTAGAGAAAGATTTTACCTGCTTATGATTAATTAATCTGCAAGAA 1320
QY  1657  AATATGATGAGCAATATATGAAATTAACACACCTTTGTTAAGATA 1704
DB   1321  AATATGATGAGCAATATATGAAATTAACACACCTTTGTTAAGATA 1368

RESULT 5
US-09-864-761-12152
: Sequence 12152, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
: FILE REFERENCE: Aeomica-X-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669

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RESULT 10
US-09-738-973-151
: Sequence 151, Application US/09738973
: Patent No. US20020110563A1
: GENERAL INFORMATION:
: APPLICANT: Reed, Steven G.
: APPLICANT: Henderson, Robert A.
: APPLICANT: Lodes, Michael J.
: APPLICANT: Fling, Steven P.
: APPLICANT: Mohamath, Raodoh
: APPLICANT: Algate, Paul A.
: APPLICANT: Secrist, Heather
: APPLICANT: Indrias, Carol Joseph
: APPLICANT: Benson, Darin R.
: APPLICANT: Elliott, Mark
: APPLICANT: Mannion, Jane
: APPLICANT: Kalos, Michael D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
: TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.475C9
: CURRENT APPLICATION NUMBER: US/09/738,973
: CURRENT FILING DATE: 2000-12-14
: NUMBER OF SEQ ID NOS: 587
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 151
: LENGTH: 3275
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-738-973-151

Query Match          4.6%; Score 78.8; DB 10; Length 3275;
Best Local Similarity 52.4%; Pred. No. 1.4e-11;
Matches 173; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

OY 479 ATTATCTCAGCAGTGTGACACCAACATTTGAACCTTTTGATGTCATGCTGAGTACA 538
DB 2445 ATTTGGTTTGATCTTCTCTGTGAAACACTTAGAGAACTTTTGATCTTACGCTGTAGA 2504
OY 539 TTTGGGGCCCCAGTATCAGTGTGATTTCTTACCTTCAGCATGATGAAGCATGAGAT 598
DB 2505 TTTATTTGCCAGTGAATGAGCATTCAGTTTTCATTTTTCACATCTTAAGCTGCGATG 2564
OY 559 GTTGAAGAGTATGTCATCTTATGCAACAATGGCAACAGCTTTCAGCATGTACAGC 658
DB 2565 AATGTGCCACGTATGTCATCTTACCTGTAAGAGAGTGTGATACACCTATGCGC 2624
OY 659 TATGAATGAAGGCAATTCAGATTCATCCAGCATTCATGCTGCTGAGTACGCCAAA 718
DB 2625 AATGATGTGCTCCAGACCAATGAACTCTGACAAATTCATGCAATTCACCTCTTCCAG 2684
OY 719 GGGGATGAGCTTTGGCTGCTGCAATGGGAGGCTCTCCATGGGGAGACCAACGCTTC 778
DB 2685 GGAGACCGAGATATGTTAGCTGTGACAGGGGAGCAATTTATGGAAGTACGGAATAT 2744
OY 779 TCCACCTTTGCAAGATTCCTGCTTTTGA 808
DB 2745 TCTAGTTTTCAGGCTATCTTCTTATCAA 2774

RESULT 11
US-09-776-976-5
: Sequence 5, Application US/09776976
: Patent No. US20020037849A1
: GENERAL INFORMATION:
: APPLICANT: Fruebis, Joachim
: APPLICANT: Erickson, Mary Ruth
: APPLICANT: Yen, Frances
: APPLICANT: Bihaui, Bernard
: TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
: FILE REFERENCE: 76.US4.REG
: CURRENT APPLICATION NUMBER: US/09/776,976
: CURRENT FILING DATE: 2001-02-05
: PRIOR APPLICATION NUMBER: US 09/758,055
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: PRIOR FILING DATE: 2001-01-10
: PRIOR APPLICATION NUMBER: US 60/176,228
: PRIOR FILING DATE: 2000-01-14
: PRIOR APPLICATION NUMBER: US 60/198,087
: PRIOR FILING DATE: 2000-04-13
: PRIOR APPLICATION NUMBER: US 60/299,881
: PRIOR FILING DATE: 2000-09-01
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: Patent.pm
: SEQ ID NO 5
: LENGTH: 4517
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-776-976-5

Query Match          4.4%; Score 74.6; DB 10; Length 4517;
Best Local Similarity 50.4%; Pred. No. 2.5e-10;
Matches 210; Conservative 0; Mismatches 204; Indels 3; Gaps 1;

OY 219 GCTTTCGAGGCTACCAAGGCCCTCTGGGCCCACCGGCCCTCTCGGCAATTCAGGAAC 278
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RESULT 12
US-09-758-055-5
: Sequence 5, Application US/09758055
: Patent No. US20020058617A1
: GENERAL INFORMATION:
: APPLICANT: Fruebis, Joachim
: APPLICANT: Erickson, Mary Ruth
: APPLICANT: Yen, Frances
: APPLICANT: Bihaui, Bernard
: TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
: FILE REFERENCE: 76.US4.REG
: CURRENT APPLICATION NUMBER: US/09/758,055
: CURRENT FILING DATE: 2001-01-10
: PRIOR APPLICATION NUMBER: US 60/176,228
: PRIOR FILING DATE: 2000-01-14
: PRIOR APPLICATION NUMBER: US 60/198,087
: PRIOR FILING DATE: 2000-04-13
: PRIOR APPLICATION NUMBER: US 60/299,881
: PRIOR FILING DATE: 2000-09-01
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: Patent.pm
: SEQ ID NO 5
: LENGTH: 4517
: TYPE: DNA
: ORGANISM: Homo sapiens
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JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1730)  
AUTHORS Maeda, T.  
TITLE Direct Submission  
JOURNAL Submitted (07-DEC-2000) Department of Radiology and Radiation  
Oncology, Graduate School of Dentistry, Osaka University, 1-8  
Yamadaoka, Suita, Osaka 565-0871, Japan  
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RESULT 2  
AX039945 1696 bp DNA linear PAT 18-NOV-2000  
LOCUS AX039945  
DEFINITION Sequence 1 from Patent W00063377.  
ACCESSION AX039945  
VERSION AX039945.1 GI:11229969  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homilidae; Homo.  
REFERENCE 1 (bases 1 to 1696)  
AUTHORS Piddington, C.S. and Bishop, P.D.  
TITLE Adipocyte complement related protein homolog zacr3  
JOURNAL Patent: WO 0063377-A 1 26-OCT-2000;  
ZymoGenetics, Inc. (US)  
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Query Match 99.1%; Score 1696; DB 6; Length 1696;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1696: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 ACCESSION AF329837  
 VERSION AF329837.1 GI:13274519  
 KEYWORDS  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1710)  
 AUTHORS Piddington, C.S. and Bishop, P.  
 TITLE Homo sapiens complement-clq tumor necrosis factor-related protein  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1710)  
 AUTHORS Piddington, C.S. and Bishop, P.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-DEC-2000) Bioinformatics, ZymoGenetics, Inc., 1201  
 Eastlake Ave. East, Seattle, WA 98102, USA  
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 Best local similarity 100.0%; Pred. No. 0;  
 Matches 1696; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Dd                    | 1395   | AATAGATTATTTAGCTTTTAAGTGCCTTGACCAGTAATATGTGGTTTAATTTTGTATATGTTCC | 1454                       |
| OY                    | 1448   | CCCACATGCCCCCACAACCTTCGGATGTGGGGTCAGAGAGTTGAGGTTCACTTTAACAAT     | 1507                       |
| Dd                    | 1455   | CCCACATGCCCCCACAACCTTCGGATGTGGGGTCAGAGAGTTGAGGTTCACTTTAACAAT     | 1514                       |
| OY                    | 1508   | GTCATAAATPATCTCATFAGGGTACGAGTGCACATAGATATTTCAAATGTTGCATGTTGACCA  | 1567                       |
| Dd                    | 1515   | GTCATAAATPATCTCATFAGGGTACGAGTGCACATAGATATTTCAAATGTTGCATGTTGACCA  | 1574                       |
| OY                    | 1568   | GAGGATTTTTATNTCTGAAGAACAATACACTATTTAATAATACCTTAGAGAAAAGATTTTGA   | 1627                       |
| Dd                    | 1575   | GAGGATTTTTATNTCTGAAGAACAATACACTATTTAATAATACCTTAGAGAAAAGATTTTGA   | 1634                       |
| OY                    | 1628   | CCTGGCTTTAGATTAATAACTGTGCGCAAGAAAAATGTAAATGACCATATTTTGCATAATAACA | 1687                       |
| Dd                    | 1635   | CCTGGCTTTAGATTAATAACTGTGCGCAAGAAAAATGTAAATGACCATATTTTGCATAATAACA | 1694                       |
| OY                    | 1688   | CACCTTTGTTAAAGAT   | 1703                       |
| Dd                    | 1695   | CACCTTTGTTAAAGAT   | 1710                       |
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| AXI36339              |  | 1709 bp  | DNA linear PAT 30-MAY-2001 |
| LOCUS                 | AXI36339   |  |                            |
| DEFINITION            | Sequence 261 from Patent EP1067182.                                    |  |                            |
| ACCESSION             | AXI36339   |  |                            |
| VERSION               | AXI36339.1 GI:14272745   |  |                            |
| KEYWORDS              |  |  |                            |
| SOURCE                | human.   |  |                            |
| ORGANISM              | Homo sapiens   |  |                            |
|                       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |  |                            |
|                       | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.              |  |                            |
| REFERENCE             | 1 (bases 1 to 1709)  |  |                            |
| AUTHORS               | Ota,T., Iseogal,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K. |  |                            |
| TITLE                 | Secretory protein or membrane protein                                  |  |                            |
| JOURNAL               | Patent: EP 1067182-A 261 10-JUN-2001;                                  |  |                            |
|                       | Helix Research Institute (JP)  |  |                            |
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|                       | PKGEKGYGIPPELQIAFMASLATHSNONGILIFSSVETIGNFFDVMTRFCAPVS                 |  |                            |
|                       | WLRFPTFSMKHEDEVEEYVYLHNHGNTVFMYSEYEMKSGDTSNHAIVKLAKGDEVEE              |  |                            |
|                       | GLRMNGCALHDDHORFTSFAGLLFETK"   |  |                            |
| BASE COUNT            | 480 a 363 c 390 g 476 t  |  |                            |
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| Query Match           | 99.0%:   | Score 1695.4:  | DB 6; Length 1709;         |
| Best Local Similarity | 99.9%:   | Pred. No. 0;   |                            |
| Matches 1696;         | Conservative 0;  | Mismatches 1;  | Indels 0; Gaps 0;          |
| OY                    | 1  | GGCATGTGCCGAGGAGGACGACGCTCTGAGACTCGCGTCTTCCAGGGAGACTCGA          | 60                         |
| Dd                    | 13   | GGCATGTGCCGAGGAGGACGACGCTCCCGGACTCTGCGTGTCTTCCAGGGAGACTCTGA      | 72                         |
| OY                    | 61   | GGCTCTGTTGAGAAATCATCTTTTGAGAGGAGCTCATCTATTGCGAACTCGCTTGTT        | 120                        |

|    |      |  |      |
|----|------|--|------|
| Db | 73   | GGCTCTGTTGAATATCATCTTTGGAGGAGCCTCATCTATTCGCAACTGCTGGCTTTGTT    | 132  |
| Qy | 121  | TTTTCTCCCTTTTTGGCTGTGTCAAGATGAATATCATGGAGTCTCCAAACCGGAGACT     | 180  |
| Db | 133  | TTTCCTCCCTTTTTGGCTGTGTCAAGATGAATATCATGGAGTCTCCAAACCGGAGACT     | 192  |
| Qy | 181  | ACCCCAAGACTGCAGTAAGTGTGTATGAGACACTACAGTTTCGAGGCTACCAAGGCC      | 240  |
| Db | 193  | ACCCCAAGACTGCAGTAAGTGTGTATGAGACACTACAGTTTCGAGGCTACCAAGGCC      | 252  |
| Qy | 241  | CCCTGGGCCCCGCGGCCCCCTGTGGCATTCGAGAAACATGAGAAACATGGCAACAATGG    | 300  |
| Db | 253  | CCCTGGGCCCCGCGGCCCCCTGTGGCATTCGAGAAACATGAGAAACATGGCAACAATGG    | 312  |
| Qy | 301  | ACCCATGCTCATGANAAGAGACCAGAAAGTGAAGAGGCGCAAGAGTGCACCTGGGCGCTCG  | 360  |
| Db | 313  | ACCCATGCTCATGANAAGAGACCAGAAAGTGAAGAGGCGCAAGAGTGCACCTGGGCGCTCG  | 372  |
| Qy | 361  | AGGGGAGCGGGGGCGACCATATGCCCCCAAGAGAGAGAAAGGCTACCCGGGATTTCCACAGA | 420  |
| Db | 373  | AGGGGAGCGGGGGCGACCATATGCCCCCAAGAGAGAGAAAGGCTACCCGGGATTTCCACAGA | 432  |
| Qy | 421  | ACTTGAGATTGCATTTCATGGCTCTCTGGCAACCCACTTCAGCAATGAGAAAGTGGAT     | 480  |
| Db | 433  | ACTTGAGATTGCATTTCATGGCTCTCTGGCAACCCACTTCAGCAATGAGAAAGTGGAT     | 492  |
| Qy | 481  | TATCTTCACAGTGTGAGACCAACATTTGGAACCTTTTGATGTCTATGATCTGTAGATT     | 540  |
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| Qy | 541  | TGGGGGCCAGTATACAGGTGTGTATTTCTTCACCTTCAGCATGATGAGCATGAGATGT     | 600  |
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| Qy | 661  | TGAAATGAAGGGCAAAATACATATCCACATCATGCTGTGCTGAAGCTAGCCAAAG        | 720  |
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| Db | 733  | GGATGAGGTTTGGCTCGAATGGGCAATGGCGCTTCATGGGAGCCCAACGCTTCTC        | 792  |
| Qy | 781  | CACCTTTGACAGATTCCTCTCTTTTGAACATTAAGTAATATATGACTAGAAATAGCTCCAC  | 840  |
| Db | 793  | CACCTTTGACAGATTCCTCTCTTTTGAACATTAAGTAATATATGACTAGAAATAGCTCCAC  | 852  |
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| Qy | 901  | GTTTTACATTGCTATATTCAAAAAATATTGTTGCAATGTGTTTCAACGCTACAGGTACA    | 960  |
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| Qy | 961  | CCAAATATGTTGACAAATTCAGGGGCTCAGAGAAATCAACCAAAATATGCTTCTCAGA     | 1020 |
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| Qy | 1021 | TGACCTTGACTAATATACAGATCTTTTTCACCTCTTCTCGGACCTTAAGATTAAT        | 1080 |
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RESULT 5  
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 ACCESSION AX191537  
 VERSION AX191537.1 GI:15209727  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 TITLE Human proteins having hydrophobic domains and dnas encoding these  
 proteins  
 JOURNAL Patent: WO 0149728-A 59 12-JUL-2001;  
 Protegene Inc. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP)  
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LOCUS BC016021
DEFINITION Homo sapiens, Similar to complement-clq tumor necrosis
factor-related protein; likely ortholog of mouse COR526
(collagenous repeat-containing sequence of 26-kDa protein), clone
MGC:27511 IMAGE:4720611, mRNA, complete cds.
ACCESSION BC016021
VERSION BC016021.1 GI:16359108
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1426)
Direct Submission
Submitted (22-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
USA.
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
Contact: amadan@systemsbio.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Kettelman and Anuradha Madan

REMARK
COMMENT
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov
Series: IRAL Plate: 38 Row: P Column: 18.
Location/Qualifiers
FEATURES

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BASE COUNT 446 a 264 c 278 g 438 t
ORIGIN
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Matches 1284; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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| Db         | 1263 | TGACCAAGAGAGATTTTATATCTGAAGAATCATACATTAATTAATTAATCTTATGAGAAAGA   | 1322 |
| Y          | 1622 | TTTTGACCTGGCTTTAGATTAATACTGTGGCAAGAAAAATGTAATGACCAATATATGANA   | 1681 |
| Db         | 1323 | TTTTGACCTGGCTTTAGATTAATACTGTGGCAAGAAAAATGTAATGACCAATATATGANA   | 1382 |
| Y          | 1682 | TAAACACACCTTTGTTAAAGATTAATAAAAAA   | 1742 |
| Db         | 1383 | TAAACACACCTTTGTTAAAGATTAATAAAAAA   | 1413 |
| RESULT 7   |      |  |      |
| AC026707   |      | 155013 bp DNA linear HTG 07-MAR-2002   |      |
| LOCUS      |      | Homo sapiens chromosome 5 clone CTD-2075C7, WORKING DRAFT SEQUENCE.  |      |
| DEFINITION |      | 2 Ordered pieces.  |      |
| ACCESSION  |      | AC026707   |      |
| VERSION    |      | AC026707.5 GI:19224781   |      |
| KEYWORDS   |      | HTG; HTGS; PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN.   |      |
| SOURCE     |      | Homo sapiens.  |      |
| ORGANISM   |      | Homo sapiens.  |      |
| REFERENCE  |      | Eukaryota; Eutherozoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.      |      |
| AUTHORS    |      | 1 (bases 1 to 155013)  |      |
| TITLE      |      | DOE Joint Genome Institute.  |      |
| JOURNAL    |      | Sequencing of Human Chromosome 5   |      |
| REFERENCE  |      | Unpublished  |      |
| JOURNAL    |      | 2 (bases 1 to 155013)  |      |
| TITLE      |      | DOE Joint Genome Institute.  |      |
| AUTHORS    |      | Direct Submission  |      |
| JOURNAL    |      | Submitted (23-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA |      |
| REFERENCE  |      | 3 (bases 1 to 155013)  |      |
| TITLE      |      | DOE Joint Genome Institute.  |      |
| AUTHORS    |      | Direct Submission  |      |
| JOURNAL    |      | Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA |      |
| COMMENT    |      | On Mar 7, 2002 this sequence version replaced gi:9256664.  |      |
|            |      | -----Genome Center   |      |
|            |      | Center: Joint Genome Institute   |      |
|            |      | Center Code: jgi   |      |
|            |      | Web site: <a href="http://www.jgi.doe.gov">http://www.jgi.doe.gov</a>  |      |

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Project Information
Center Project Name: 656404
Center clone name: CITB-H1_2075C7
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Summary Statistics
Consensus quality: 153352 bases at least Q40
Consensus quality: 154674 bases at least Q30
Consensus quality: 154871 bases at least Q20
Estimated insert size: 171000: pulse field gel estimation
Estimated insert size: 154913: sum-of-contrigs estimation
Quality coverage: 9.64 in Q20 bases: pulse field gel estimation
Quality coverage: 10.64 in Q20 bases: sum-of-contrigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 6677: contig of 6677 bp in length
* 6678 6777: gap of unknown length
* 6778 155013: contig of 148256 bp in length.
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/chromosome="5"
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/clone_lib="Caltech human BAC library D"
BASE COUNT 44427 a 31256 c 31672 g 47558 t 100 others
ORIGIN
Query Match 61.4%: Score 1050.8; DB 2; Length 155013;
Best Local Similarity 99.8%: Pred. No. 5.1e-25;
Matches 1052; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 651 TGTCACGCTATGAATGAAGGGCAATCAGATACATCCAGCAATCATGCTGCTGAAGC 710
DB 67831 TTTCCAGCTATGAATGAAGGGCAATCAGATACATCCAGCAATCATGCTGCTGAAGC 67890
QY 711 TAGCCAAAGGGGATGAGCTTTGGCTGCGCAATGCGCAATGCGGCTCTCCATGGGGACAC 770
DB 67891 TAGCCAAAGGGGATGAGCTTTGGCTGCGCAATGCGGCAATGCGGCTCTCCATGGGGACAC 67950
QY 771 AACGCTTCCACACCTTTGACGATTCGCTCTTTGGAACATGAAATATATGACTAGA 830
DB 67951 AACGCTTCCACACCTTTGACGATTCGCTCTTTGGAACATGAAATATATGACTAGA 68010
QY 831 ATAGCTCCACTTTGGGGAGAAGCTGTAGCTGAGCTGATTTGTTACGATCTGAGAACATT 890
DB 68011 ATAGCTCCACTTTGGGGAGAAGCTGTAGCTGAGCTGATTTGTTACGATCTGAGAACATT 68070
QY 891 AAGGTGAGGGTTTTACATGCTGATTCAGAAAATTTATGGTGCAATGTTGTTCAAGC 950
DB 68071 AAGGTGAGGGTTTTACATGCTGATTCAGAAAATTTATGGTGCAATGTTGTTCAAGC 68130
QY 951 TACAGGTACACCAATTAAGTTGGACAATTCAGGGGCTCAGAGAATCAACCACAAAATAG 1010
DB 68131 TACAGGTACACCAATTAAGTTGGACAATTCAGGGGCTCAGAGAATCAACCACAAAATAG 68190
QY 1011 TCTTCTCAGATGACCTTGACATATATATCTCAGCATCTTTATCAGCTCTTCTTGACACT 1070
DB 68191 TCTTCTCAGATGACCTTGACATATATATCTCAGCATCTTTATCAGCTCTTCTTGACACT 68250
QY 1071 AAAAGATTAATCTCCTCGAGGACGCTGGAAATATTTTTTTCATCAGAGAATCATTT 1130
DB 68251 AAAAGATTAATCTCCTCGAGGACGCTGGAAATATTTTTTTCATCAGAGAATCATTT 68310
QY 1131 GCAAGAAATTTGACTACTGCTTTTAAATTAAATACAGTTTTCAGGACCCCTGGAAGT 1190
DB 68310 GCAAGAAATTTGACTACTGCTTTTAAATTAAATACAGTTTTCAGGACCCCTGGAAGT 1190

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Db 11147 AATTGTGTATGTTCCCGCCACATGCGCCCAACTTCGGATGTGGCGTGAAGGTTGAG 11206
OY 1491 GTTCACATATAACAATGTCAATAATATCTCATAGAGTACAGTGGCCATAGATATTCAA 1550
Db 11207 GTTCACATATAACAATGTCAATAATATCTCATAGAGTACAGTGGCCATAGATATTCAA 11266
OY 1551 ATGTGCATGTGACAGAGGGATTTATATCTGAAGAATACACTATATTAATAATACC 1610
Db 11267 ATGTGCATGTGACAGAGGGATTTATATCTGAAGAATACACTATATTAATAATACC 11326
OY 1611 TTAGAGAAAGATTTTGACCTGGCTTATAGATAAAGTGTGCAAGAAATATTAATGAGA 1670
Db 11327 TTAGAGAAAGATTTTGACCTGGCTTATAGATAAAGTGTGCAAGAAATATTAATGAGA 11386
OY 1671 ATATATGGAATAAACAACACTTTGTTAAAGATA 1704
Db 11387 ATATATGGAATAAACAACACTTTGTTAAAGATA 11420

RESULT 9
AX136588 810 bp DNA linear PAT 30-MAY-2001
LOCUS AX136588
DEFINITION Sequence 510 from Patent EP1067182.
ACCESSION AX136588
VERSION AX136588.1 GI:14272992
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 810)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: EP 1067182-A 510 10-JAN-2001;
Helix Research Institute (JP)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 200 a 201 c 218 g 188 t 3 others
ORIGIN
Query Match 44.8%; Score 766.6; DB 6; Length 810;
Best Local Similarity 98.9%; Pred. No. 3.4e-183;
Matches 791; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

OY 1 GGCATCTGCCGAGAGACACGCTCTGGAGCTCTGCTGCTCTCCAGAGGAGACTCTGA 60
Db 13 GGCATCTGCCGAGAGACACGCTCTGGAGCTCTGCTGCTCTCCAGAGGAGACTCTGA 72
OY 61 GGCCTGTGTGAATCATGCTTTGGAGGCACTCATATTGCAACACTGCTGGCTTTGTT 120
Db 73 GGCCTGTGTGAATCATGCTTTGGAGGCACTCATATTGCAACACTGCTGGCTTTGTT 132
OY 121 TTTCTCTCTTTTCCCTGCTGTGCAAGATGATACATGAGTCTCCACAACCGAGAGACT 180
Db 133 TTTCTCTCTTTTCCCTGCTGTGCAAGATGATACATGAGTCTCCACAACCGAGAGACT 192
OY 181 ACCCCACAGTGCATAGTGTGTTCATGAGACTACAGCTTTGAGAGCTTACCAAGGCC 240
Db 193 ACCCCACAGTGCATAGTGTGTTCATGAGACTACAGCTTTGAGAGCTTACCAAGGCC 252
OY 241 CCGTGGCCACCGGCGCTCTGCGCATTCAGGAACCATGGAACCAATGCAACATG 300
Db 253 CCGTGGCCACCGGCGCTCTGCGCATTCAGGAACCATGGAACCAATGCAACATG 312
OY 301 AGCCACTGTGTGAAGAGCCAAAGGTGAGAGGGCGCAAAAGTGTGACCTGGCCCTG 360
Db 313 AGCCACTGTGTGAAGAGCCAAAGGTGAGAGGGCGCAAAAGTGTGACCTGGCCCTG 372
OY 361 AGGGAAGGGGGGCGAGCATGGCCCAAGAGAGAGAGGGCTACCGGGGATTCCACAGA 420
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Db 373 AGGGAGCGGGGGCGACATGCGCCCAAGAGAGAGAGGGCTACCGGGGATTCACACAGA 432
OY 421 ACTTCAGATTTGATTCATGAGCTTCTCTGCGCAACCCACTTCAGCAATCAGAACAGTGGAT 480
Db 433 ACTTCAGATTTGATTCATGAGCTTCTCTGCGCAACCCACTTCAGCAATCAGAACAGTGGAT 492
OY 481 TATCTTCAGACATGTGTTGAGACCAACATTGGAAACTTTGATGATCATGCTGATGATT 540
Db 493 TATCTTCAGACATGTGTTGAGACCAACATTGGAAACTTTGATGATCATGCTGATGATT 552
OY 541 TGGGGGCCAGATGATGAGGTGTGATTTCTTCACCTTCAGCATGATGATGATGATGATG 600
Db 553 TGGGGGCCAGATGATGAGGTGTGATTTCTTCACCTTCAGCATGATGATGATGATGATG 612
OY 601 TGAGGAAGTGTATGTATGATCTTATGACAAATGCGCAACAGCTTCAGCATGATGATGATG 660
Db 613 TGAGGAAGTGTATGTATGATCTTATGACAAATGCGCAACAGCTTCAGCATGATGATGATG 672
OY 661 TGAATGAAGGCAATCATGATACATCCAGCAATCATGCTGTGCTGAGAGCTAGCCAAAG 720
Db 673 TGAATGAAGGCAATCATGATACATCCAGCAATCATGCTGTGCTGAGAGCTAGCCAAAG 731
OY 721 GGATGAGGTTTGGCTGCGCAATGCGCAATGCGCTCTCCATGGGGAGCCACCAAGCTTCTC 780
Db 732 GGATGAGGTTTGGCTGCGCAATGCGCAATGCGCTCTCCATGGGGAGCCACCAAGCTTCTC 790
OY 781 CACTTTCGAGGATTCCTGC 800
Db 791 CACTTTCGAGGATTCCTGC 810

RESULT 10
AX039955 1117 bp DNA linear PAT 18-NOV-2000
LOCUS AX039955
DEFINITION Sequence 11 from Patent WO0063377.
ACCESSION AX039955
VERSION AX039955.1 GI:11229976
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 1117)
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Piddington,C.S. and Bishop,P.D.
JOURNAL Adipocyte complement related protein homolog zacrp3
ZymoGenetics, Inc. (US)
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Source 1. 1117
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/db_xref="taxon:10090"
111. 851
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/codon_start=1
/protein_id="CAC16633.1"
/db_xref="GI:11229977"
/translational="MLGRORIWMHLPLPLPFLCOCDEYMESPQAGLPPDCSKCH
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PKGEGKGYGVPPELOIAPMASLATHFNSONGSIISSVETNIGNFPDMTRFAPYS
GVYFRTSMKHHEDEVEVYIYLMHNGNTVSMYSEYTKGKSDTSSNHNVLAKDEV
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BASE COUNT 284 a 272 c 293 g 268 t
ORIGIN
Query Match 40.6%; Score 695.8; DB 6; Length 1117;
Best Local Similarity 85.5%; Pred. No. 3e-165;
Matches 786; Conservative 0; Mismatches 132; Indels 1; Gaps 1;
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QY 132 TTTCCTGTGTCAAGATGATGAGTCTCCACAACCGAGAGACTACCCCACT 191  
 DB 166 TTTCCTGTGTCAAGATGATGAGTCTCCACAACCGAGAGACTACCCCACT 225  
 QY 192 GCAGTAACTGTCTCAGAGACTACAGCTTTGAGGCTACCAAGCCCTCGGCGAC 251  
 DB 226 GCAGTAACTGTCTCAGAGACTACAGCTTTGAGGCTACCAAGCCCTCGGCGAC 285  
 QY 252 CGGCGCTCTCTGCTTCCAGAACCATGGAACATGCAATGCAATGAGCCCTGCTC 311  
 DB 286 CAGGTCTCTCTGCTTCCAGAACCATGGAACATGCAATGCAATGAGCCCTGCTC 345  
 QY 312 ATGAAGAGCCAAAGGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 371  
 DB 346 ATGAAGAGCCAAAGGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405  
 QY 372 GCGAGCATGCCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431  
 DB 406 GCGAGCATGCCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465  
 QY 432 CATTGATGCTCTCTGCTTCCAGAACCATGGAACATGCAATGCAATGAGCCCTGCTC 491  
 DB 466 CATTGATGCTCTCTGCTTCCAGAACCATGGAACATGCAATGCAATGAGCCCTGCTC 525  
 QY 492 GTGTGAGACCAACATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 551  
 DB 526 GTGTGAGACCAACATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 585  
 QY 552 TATCAGCTGTGTATTTCTTCCAGCTTACAGATGATGAAGATGAGATGAGAGACTGT 611  
 DB 586 TATCAGCTGTGTATTTCTTCCAGCTTACAGATGATGAAGATGAGATGAGAGACTGT 645  
 QY 612 ATGTGACCTTATGCAACATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 671  
 DB 646 ATGTGACCTTATGCAACATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 705  
 QY 672 GCAATCAGATATCATCAGACATCATCTGTGTGAGAGTACGAGAGAGAGAGAGCTTT 731  
 DB 706 GAAATCAGATATCATCAGACATCATCTGTGTGAGAGTACGAGAGAGAGAGAGCTTT 765  
 QY 732 GCGTGGATGAG 791  
 DB 766 GCGTGGATGAG 825  
 QY 792 GATTCCGCTTGTGAACATGATATATGATGATGATGATGATGATGATGATGATG 851  
 DB 826 GATTCCGCTTGTGAACATGATATATGATGATGATGATGATGATGATGATGATG 885  
 QY 852 CTGTGAGCTGAGCT-GATTTGTTACGATCTGAGAGACATTAAGTTGAGGCTTTTACATT 910  
 DB 886 TTATATGCTGAGCTGAGGCTTTGAGATATGAGAGATGTTGAAGTGGGGCTTTTATG 945  
 QY 911 GCTGTATTCAAAAAATTTATGTTGCAATGTTTTCACGCTACAGTACCAATTAATGT 970  
 DB 946 GACCATTTAAGTCTTGTGATGCTGACACACTCTACTCTAATGATGATGATGATGATG 1005  
 QY 971 TGGACATTCAGGGGCTCA 989  
 DB 1006 TGGATGCTTCAGGGGCTCA 1024

RESULT 11  
 AF246265 1879 bp mRNA linear ROD 29-JAN-2001  
 LOCUS AF246265  
 DEFINITION Mus musculus collagenous repeat-containing sequence of 26kDa  
 ACCESSION AF246265  
 VERSION AF246265.1 GI:11275676  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus.  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1879)  
 AUTHORS Maeda,T., Abe,M., Kurisu,K., Jikko,A. and Furukawa,S.  
 TITLE Molecular cloning and characterization of a novel gene, COR526, encoding a putative secretory protein and its possible involvement in skeletal development  
 JOURNAL J. Biol. Chem. 276 (5), 3628-3634 (2001)  
 MEDLINE 21264842  
 PUBMED 11071891  
 REFERENCE 2 (bases 1 to 1879)  
 AUTHORS Maeda,T. and Jikko,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-MAR-2000) Radiology and Radiation Oncology, Osaka University School of Dentistry, 1-8 Yamadaoka, Suita, Osaka 565-0871, Japan  
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 source location/Qualifiers  
 1. 1879  
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 BASE COUNT 536 a 409 c 426 g 508 t  
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 Query Match 40.5%; Score 694.2; DB 10; Length 1879;  
 Best Local Similarity 85.4%; Pred. No. 7.9e-165;  
 Matches 785; Conservative 0; Mismatches 133; Indels 1; Gaps 1;  
 QY 72 GAATCATGCTTTGGAGGAGCTCATCTATTGGCACTGCTGCTTTTCTCTCCCTT 131  
 DB 95 GACCATGCTCGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 154  
 QY 132 TTTCCTGTGTCAAGATGATGAGTCTCCACAACCGAGAGACTACCCCACT 191  
 DB 155 TTTCCTGTGTCAAGATGATGAGTCTCCACAACCGAGAGAGACTACCCCACT 214  
 QY 192 GCAGTAACTGTCTCAGAGACTACAGCTTTGAGGCTACCAAGCCCTCGGCGAC 251  
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 QY 252 CGGCGCTCTCTGCTTCCAGAACCATGGAACATGCAATGCAATGAGCCCTGCTC 311  
 DB 275 CAGGTCTCTCTGCTTCCAGAACCATGGAACATGCAATGCAATGAGCCCTGCTC 334  
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 QY 372 GCGAGCATGCCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431  
 DB 395 GCGAGCATGCCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 454  
 QY 432 CATTGATGCTCTCTGCTTCCAGAACCATGGAACATGCAATGCAATGAGCCCTGCTC 491  
 DB 455 CATTGATGCTCTCTGCTTCCAGAACCATGGAACATGCAATGCAATGAGCCCTGCTC 514  
 QY 492 GTGTGAGACCAACATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 551  
 DB 515 GTGTGAGACCAACATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 574  
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Db 482 ATTGAGAGAAATCGGATGATGATG- CAGGGCTGGGGCAAGAACAGGGGCACTACT 424  
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Db 363 ATCCAGAAAATACATTTAAATCTGAAATTCACATACATGCTATTTTAAAGCATAGAT 304  
Oy 1395 TTATAGTAAAGTCTGTCAGCAGTAAATGTTGTAATTTTGTGATGTTCCCCACAT 1454  
Db 303 TTATAGTAAAGTCTGTCAGCAGTAAATGTTGTAATTTTGTGATGTTCCCCACAT 244  
Oy 1455 CCCCCCACTTGGAGTGGGGTCAGAGAGTTCAGTCTATTAACAATGTCATTA 1514  
Db 243 CCCCCCACTTGGAGTGGGGTCAGAGAGTTCAGTCTATTAACAATGTCATTA 184  
Oy 1515 ATATCTATAGAGGTAGAGTCCCATATAGATATTCAAATGTTGATGACAGAGGAT 1574  
Db 183 ATATCTATAGAGGTAGAGTCCCATATAGATATTCAAATGTTGATGACAGAGGAT 124  
Oy 1575 TTATATCTGAAGACATACATATTAATTAATACCTTAGAGAAAGATTGACCTGGCT 1634  
Db 123 TTATATCTGAAGACATACATATTAATTAATACCTTAGAGAAAGATTGACCTGGCT 64  
Oy 1635 TTAGATAAACTGTGGCAAGAAATGTAATGAGCAATATATGGAATTAACACACCTTT 1694  
Db 63 TTAGATAAACTGTGGCAAGAAATGTAATGAGCAATATATGGAATTAACACACCTTT 4  
Oy 1695 GTT 1697  
Db 3 GTT 1  
RESULT 14  
AX191527 672 bp DNA linear PAT 15-AUG-2001  
LOCUS AX191527  
DEFINITION Sequence 49 from Patent WO0149728.  
ACCESSION AX191527  
VERSION AX191527.1 GI:15209709  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Kato, S. and Kimura, T.  
TITLE Human proteins having hydrophobic domains and dnas encoding these  
proteins  
JOURNAL Patent: WO 0149728-A 49 12-JUL-2001;  
Proteome Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP)  
FEATURES  
source 1. .672  
Location/Qualifiers  
BASE COUNT 185 a 170 c 187 g 130 t  
ORIGIN  
Query Match 21.1%; Score 361; DB 6; Length 672;  
Best Local Similarity 100.0%; Pred. No. 1.9e-80;  
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 422 ATGGAACAAATGGCAACAAATGAGCCACATGCTCATGAAGAGACCAAGGTGAAGGGCG 481  
Oy 339 ACAAGGTGACCTGGGGCTTCGAGGGAGCGGGGACAGATGGCCCAAGAGAGAGG 398  
Db 482 ACAAGGTGACCTGGGGCTTCGAGGGAGCGGGGACAGATGGCCCAAGAGAGAGG 541  
Oy 399 GCTACCGGGGATTCACACAGAACTTCAATGATTCATGCTTCTGCAACCCACT 458  
Db 542 GCTACCGGGGATTCACACAGAACTTCAATGATTCATGCTTCTGCAACCCACT 601  
Oy 459 TCAGCAATCAGAACAGTGGATTTATCTTCAGCAGTTCAGACCAACATTTGAACCTCT 518  
Db 602 TCAGCAATCAGAACAGTGGATTTATCTTCAGCAGTTCAGACCAACATTTGAACCTCT 661  
Oy 519 T 519  
Db 662 T 662  
RESULT 15  
AX079496 546 bp DNA linear PAT 22-FEB-2001  
LOCUS AX079496  
DEFINITION Sequence 240 from Patent WO0107611.  
ACCESSION AX079496  
VERSION AX079496.1 GI:13159056  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Baker, K.P., Goddard, A. and Wood, W.I.  
TITLE Human polypeptides and methods for the use thereof  
JOURNAL Patent: WO 0107611-A 240 01-FEB-2001;  
Genentech, Inc. (US)  
FEATURES  
source 1. .546  
Location/Qualifiers  
BASE COUNT 149 a 129 c 155 g 108 t 5 others  
ORIGIN  
Query Match 12.1%; Score 208; DB 6; Length 546;  
Best Local Similarity 99.5%; Pred. No. 1.1e-41;  
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: January 15, 2003, 18:56:35  
Job time : 4496 secs





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source
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/db_xref="taxon:9606"
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/cell_line="H1080"
/Note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
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method was used, these sequence tags are not necessarily
expressed in H1080 under normal circumstances."
BASE COUNT      220 a      156 c      165 g      234 t      1 others
ORIGIN

Query Match      43.9%; Score 751.8; DB 12; Length 776;
Best Local Similarity 99.6%; Pred. No. 2.3e-174;
Matches 764; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Oy 428 ATTGCATTCATGCTCTCTGCGACCCACTTGCAGCAATCAGAACAGTGGATTATCTTC 487
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Db 1  ATTGCATTCATGCTCTCTCTGCGACCCACTTGCAGCAATCAGAACAGTGGATTATCTTC 60

Oy 488 AGCAGTGTGAGACCAACATTTGAACTTCTTGATGTCATGACTGTGATTTGGGGCC 547
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Db 61  AGCAGTGTGAGACCAACATTTGAACTTCTTGATGTCATGACTGTGATTTGGGGCC 120

Oy 548 CCACTATCAGGTGTATTTCTTCACTTACGATGATGAAGATGAGATGTTGAGAA 607
    |||||||
Db 121 CCACTATCAGGTGTATTTCTTCACTTACGATGATGAAGATGAGATGTTGAGAA 180

Oy 608 GTTATGTGACCTTTCAGCAATGGCAACAGTCTTCAGCATGTACATGATGAATG 667
    |||||||
Db 181 GTTATGTGACCTTTCAGCAATGGCAACAGTCTTCAGCATGTACATGATGAATG 240

Oy 668 AAGGCAAAATCAGATACATCCAGCAATCATGCTGTGTAAGTGAAGGAGATGAG 727
    |||||||
Db 241 AAGGCAAAATCAGATACATCCAGCAATCATGCTGTGTAAGTGAAGGAGATGAG 300

Oy 728 GTTGGCTGGGAATGGGCATGGCGCTCTCCATGGGGACCAACGCTTCTCCACTTT 787
    |||||||
Db 301 GTTGGCTGGGAATGGGCATGGCGCTCTCCATGGGGACCAACGCTTCTCCACTTT 360

Oy 788 GCGAGATTCCTGCTCTTTCGAACTAATATATATGACTAGATAGATCTCCATTTGGG 847
    |||||||
Db 361 GCGAGATTCCTGCTCTTTCGAACTAATATATATGACTAGATAGATCTCCATTTGGG 420

Oy 848 AAGACTGTGAGCTGAGCTGATTTGTACGATCTGAGGAACATTAAAGTTGAGGGTTTAC 907
    |||||||
Db 421 AAGACTGTGAGCTGAGCTGATTTGTACGATCTGAGGAACATTAAAGTTGAGGGTTTAC 480

Oy 908 ATTGCTATATCAAAAATATATGTTGTGCAATGTGTTCAAGCTACAGCTACACATTA 967
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Db 481 ATTGCTATATCAAAAATATATGTTGTGCAATGTGTTCAAGCTACAGCTACACATTA 540

Oy 968 TGTTCGACATTCAGGGCTCAGAGAATCAACCAAAAATAGTCTCTCAGATGACCTT 1027
    |||||||
Db 541 TGTTCGACATTCAGGGCTCAGAGAATCAACCAAAAATAGTCTCTCAGATGACCTT 600

Oy 1028 GACTAATATATCTGACATCTTATCTCTTTCCTTGGCACCTTAAGATATATCTCTC 1087
    |||||||
Db 601 GACTAATATATCTGACATCTTATCTCTTTCCTTGGCACCTTAAGATATATCTCTC 660

Oy 1088 TGACGAGGTGGAATATTTTCTATCAGAGAAGTCATTTGCAAGAATTTTGACTA 1147
    |||||||
Db 661 TGACGAGGTGGAATATTTTCTATCAGAGAAGTCATTTGCAAGAATTTTGACTA 720

Oy 1148 CTCGCTTTAATTTATACAGTTTCAGGAACCCCTGAAGTTTA 1194
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Db 721 CTCGCTTTAATTTATATACAGTTTCAGGAACCCCTGAAGTTTA 766

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RESULT 2  
BG186928/c

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LOCUS      BG186928      874 bp      mRNA      linear      EST 21-APR-2001
DEFINITION RSTS905 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG186928
VERSION    BG186928.1  GI:13708615
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 874)
            Harrington,J.V., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
            Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
            ,E., Veloso,N., Kliska,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
            Creation of genome-wide protein expression libraries using random
            activation of gene expression
            Nat. Biotechnol. 19 (5), 440-445 (2001)
JOURNAL    2127151
MEDLINE    Contact: Scott J. Cain
COMMENT    Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@atersys.com
            High quality sequence stop: 522.
            Location/Qualifiers
                source
                1. .874
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="Athersys RAGE Library"
                /cell_line="H1080"
                /Note="See 'Creation of Genome-wide Protein Expression
                Libraries using Random Activation of Gene Expression',
                Nature Biotechnology, in press. Note that even though the
                cell type indicated is H1080, since a random activation
                method was used, these sequence tags are not necessarily
                expressed in H1080 under normal circumstances."
BASE COUNT      276 a      168 c      162 g      268 t
ORIGIN

Query Match      43.4%; Score 743.4; DB 12; Length 874;
Best Local Similarity 94.7%; Pred. No. 2.8e-172;
Matches 802; Conservative 0; Mismatches 41; Indels 4; Gaps 3;

Oy 843 TGGGGAAGACTTGTAGCTGAGCTGATTTGTACGATCTGAGGAACATTAAAGTTGAGGT 902
    |||||
Db 856 TTGGGGAACCTAGTAGCTGAGTTAATTTGT--CCTTTTCGGAACCAATAAAGTTGGGG 799

Oy 903 TTTCATTTGCTGTATTCAAAATATATTTGTCATGTTTTCACGCTACAGSTA-CAC 961
    |||||
Db 798 TTTCATGCTGTATTTAAAATATATTTGGTCGAATGTTGTCTCCGTCACAGGACCCC 739

Oy 962 CAATATATGTTGACATTCAGGGGCTCAGAGAATCAACCAAAAATAGTCTCTCAGAT 1021
    |||||
Db 738 CAATATATGTTGCAATTCAGGGGCTCAGAAAATCACCCAC-AAATAGTTTTTCAGAT 680

Oy 1022 GACCTTACATATATCTGACATCTTATCAGATCTTCTTGGCACCTTAAGATATAT 1081
    |||||
Db 679 GACTTTGATTAATTAACCTGACATCTTATCAGATCTTCTTGGCACCTTAAGATATAT 620

Oy 1082 CTCCTGACGAGGTGGAATATTTTTCATCAAGAGTCAATTCGCAAGAAATTT 1141
    |||||
Db 619 CTCCTGACGAGGTGGAATATTTTTCATCAAGAGTCAATTCGCAAGAAATTT 560

Oy 1142 TGACTACTGCTTTTAAATTAATACAGTTTTCAGGAACCCCTGAAGTTTAAGTTCA 1201
    |||||
Db 559 TGACTACTGCTTTTAAATTAATACAGTTTTCAGGAACCCCTGAAGTTTAAGTTCA 500

Oy 1202 TATTCCTTAATACATTTGAGAGATTCGATGATGATGATGAGAGGCTGGGGCAAGAC 1261
    |||||
Db 499 TATTCCTTAATACATTTGAGAGATTCGATGATGATGATGAGAGGCTGGGGCAAGAC 440

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| LOCUS      | DEFINITION  | ACCESSION | VERSION | KEYWORDS        | SOURCE | ORGANISM | REFERENCE | AUTHORS | JOURNAL | COMMENT |
|------------|---|-----------|---------|-----------------|--------|----------|-----------|---------|---------|---------|
| Oy 1262    | AGGGGCACTAGCTGCTTATAGCAATTAATTTAGTGGCCCTCCGTACACTTAGCCTTTGA         | 1321      |         |                 |        |          |           |         |         |         |
| Db 439     | AGGGGCACTAGCTGCTTATAGCAATTAATTTAGTGGCCCTCCGTACACTTAGCCTTTGA         | 380       |         |                 |        |          |           |         |         |         |
| Oy 1322    | CCCTTCCCTTTTGATGCCACAAATATCATTAATAACTCTGAATTACATACATACATATTTT       | 1381      |         |                 |        |          |           |         |         |         |
| Db 379     | CCCTTCCCTTTTGATGCCACAAATATCATTAATAACTCTGAATTACATACATACATATTTT       | 320       |         |                 |        |          |           |         |         |         |
| Oy 1382    | AAAGTCATATAGATTTTACCTATAAAGTCTTGACACAGTAATGTGGTTGATTTGTGTGA         | 1441      |         |                 |        |          |           |         |         |         |
| Db 319     | AAAGTCATATAGATTTTACCTATAAAGTCTTGACACAGTAATGTGGTTGATTTGTGTGA         | 260       |         |                 |        |          |           |         |         |         |
| Oy 1442    | TGTTTCCCCCAGTATGCGCCCAACTCTGGATGTGGGGGTAGAGAGTTGAGTTCACTATTA        | 1501      |         |                 |        |          |           |         |         |         |
| Db 239     | TGTTTCCCCCAGTATGCGCCCAACTCTGGATGTGGGGGTAGAGAGTTGAGTTCACTATTA        | 200       |         |                 |        |          |           |         |         |         |
| Oy 1502    | ACAAATGTCAATTAATATCTAGAGATGATGAGTGCATTAATTAATTAATTAATTAATTAAT       | 1561      |         |                 |        |          |           |         |         |         |
| Db 139     | ACAAATGTCAATTAATATCTAGAGATGATGAGTGCATTAATTAATTAATTAATTAATTAAT       | 140       |         |                 |        |          |           |         |         |         |
| Oy 1562    | TGACACAGAGGAGTATTTATATCTGAAGAACAATACACTATTAATTAATTAATTAATTAAT       | 1621      |         |                 |        |          |           |         |         |         |
| Db 139     | TGACACAGAGGAGTATTTATATCTGAAGAACAATACACTATTAATTAATTAATTAATTAAT       | 80        |         |                 |        |          |           |         |         |         |
| Oy 1622    | TTTTTACCTGCTTATAGTATAAACTGTGGCGAAGAAAAATGTATATGACAATATATGCAAA       | 1681      |         |                 |        |          |           |         |         |         |
| Db 79      | TTTTTACCTGCTTATAGTATAAACTGTGGCGAAGAAAAATGTATATGACAATATATGCAAA       | 20        |         |                 |        |          |           |         |         |         |
| Oy 1682    | TAAACAC 1688  |           |         |                 |        |          |           |         |         |         |
| Db 19      | TAAACAC 13  |           |         |                 |        |          |           |         |         |         |
| RESULT 3   |   |           |         |                 |        |          |           |         |         |         |
| BM924169   | 1103 bp   | MRNA      | linear  | EST 12-MAR-2002 |        |          |           |         |         |         |
| DEFINITION | AGNCOCORT.6630535 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760396 |           |         |                 |        |          |           |         |         |         |
| ACCESSION  | BM924169  |           |         |                 |        |          |           |         |         |         |
| VERSION    | BM924169.1  |           |         |                 |        |          |           |         |         |         |
| KEYWORDS   | EST.  |           |         |                 |        |          |           |         |         |         |
| SOURCE     | human.  |           |         |                 |        |          |           |         |         |         |
| ORGANISM   | Homo sapiens  |           |         |                 |        |          |           |         |         |         |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |           |         |                 |        |          |           |         |         |         |
| AUTHORS    | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.          |           |         |                 |        |          |           |         |         |         |
| JOURNAL    | 1 (bases 1 to 1103)   |           |         |                 |        |          |           |         |         |         |
| COMMENT    | NIH-MGC http://mgc.nci.nih.gov/;                                    |           |         |                 |        |          |           |         |         |         |
|            | National Institutes of Health, Mammalian Gene Collection (MGC)      |           |         |                 |        |          |           |         |         |         |
|            | Unpublished (1999)  |           |         |                 |        |          |           |         |         |         |
|            | Contact: Robert Strausberg, Ph.D.                                   |           |         |                 |        |          |           |         |         |         |
|            | Email: c9apbs-remail.nih.gov  |           |         |                 |        |          |           |         |         |         |
|            | Tissue Procurement: Life Technologies, Inc.                         |           |         |                 |        |          |           |         |         |         |
|            | cDNA Library Preparation: Life Technologies, Inc.                   |           |         |                 |        |          |           |         |         |         |
|            | cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)            |           |         |                 |        |          |           |         |         |         |
|            | DNA Sequencing by: Agencourt Bioscience Corporation                 |           |         |                 |        |          |           |         |         |         |
|            | Clone distribution: MGC clone distribution information can be       |           |         |                 |        |          |           |         |         |         |
|            | found through the I.M.A.G.E. Consortium/LNL at:                     |           |         |                 |        |          |           |         |         |         |
|            | http://image.llnl.gov   |           |         |                 |        |          |           |         |         |         |
|            | Plate: LLAM12807 row: f column: 13                                  |           |         |                 |        |          |           |         |         |         |
|            | High quality sequence stop: 564.                                    |           |         |                 |        |          |           |         |         |         |
| FEATURES   | Location/Qualifiers   |           |         |                 |        |          |           |         |         |         |
| SOURCE     | 1. 1103   |           |         |                 |        |          |           |         |         |         |
|            | /organism="Homo sapiens"  |           |         |                 |        |          |           |         |         |         |
|            | /db_xref="taxon:9606"   |           |         |                 |        |          |           |         |         |         |
|            | /clone="IMAGE:5760396"  |           |         |                 |        |          |           |         |         |         |
|            | /clone_1lb="NIH_MGC_116"  |           |         |                 |        |          |           |         |         |         |
|            | /lab_host="DH10B"   |           |         |                 |        |          |           |         |         |         |

| Query Match                           | Best Local Similarity | Matches | Conservative | Score | DB       | Length |
|---------------------------------------|-----------------------|---------|--------------|-------|----------|--------|
| 41.1%                                 | 91.9%                 | 0       | 56           | 20    | 103      |        |
| Destroyed upon cloning.               |                       |         |              |       |          |        |
| Average insert size 1.4 kb,           |                       |         |              |       |          |        |
| insert size range 1-3 kb.             |                       |         |              |       |          |        |
| Library is normalized and             |                       |         |              |       |          |        |
| enriched for full-length clones       |                       |         |              |       |          |        |
| and was constructed by C.             |                       |         |              |       |          |        |
| Gruber (Invitrogen).                  |                       |         |              |       |          |        |
| Research Genetics tracking code       |                       |         |              |       |          |        |
| 023. Note: this is a NIH-MC Library." |                       |         |              |       |          |        |
| BASE COUNT                            | 274 a                 | 285 c   | 279 g        | 264 t | 1 others |        |
| ORIGIN                                |                       |         |              |       |          |        |
| Query Match                           | Best Local Similarity | Matches | Conservative | Score | DB       | Length |
| 41.1%                                 | 91.9%                 | 0       | 56           | 20    | 103      |        |
| Destroyed upon cloning.               |                       |         |              |       |          |        |
| Average insert size 1.4 kb,           |                       |         |              |       |          |        |
| insert size range 1-3 kb.             |                       |         |              |       |          |        |
| Library is normalized and             |                       |         |              |       |          |        |
| enriched for full-length clones       |                       |         |              |       |          |        |
| and was constructed by C.             |                       |         |              |       |          |        |
| Gruber (Invitrogen).                  |                       |         |              |       |          |        |
| Research Genetics tracking code       |                       |         |              |       |          |        |
| 023. Note: this is a NIH-MC Library." |                       |         |              |       |          |        |
| BASE COUNT                            | 274 a                 | 285 c   | 279 g        | 264 t | 1 others |        |
| ORIGIN                                |                       |         |              |       |          |        |

```

Db      901 CTTGGCTGACTCAAAAATTAATTGCTTGGGAG 934
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RESULT 4
BG201468
LOCUS   BG201468
DEFINITION BG201468 762 bp mRNA linear EST 21-APR-2001
ACCESSION R8220685 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.
VERSION   BG201468.1 GI:13723043
KEYWORDS EST.
SOURCE    human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS  Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
1 (bases 1 to 762)
Harrington,J.J., Thornton,M., Ramachandran,R., Whittington,J.,
Cain,S., Leventhal,C., Costanzo,D., McElligott,K., Boozar,S., Mays,R., Smith
,J., Danzig,J. and Ducar,M.
'E., Veloso,N., Klika,A., Hess,J., Coltrien,K., Lo,K., Offenbacher
activation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
TITLE
JOURNAL  Contact: Scott J. Cain
MEDLINE  Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
COMMENT  High quality sequence stop: 504.
Location/Qualifiers
1. 762
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT 218 a 154 c 162 g 228 t
ORIGIN
Query Match 40.5% Score 692.6; DB 12; Length 762;
Best Local Similarity 98.3%; Pred. No. 8.8e-160;
Matches 742; Conservative 0; Mismatches 9; Indels 4; Gaps 4;

QY 428 ATTGCATTCATGGCTCTCTGCGCAACCCACTTCAGCAATCAGACAGTGGATATCTTC 487
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Db 1 ATTGCATTCATGGCTCTCTGCGCAACCCACTTCAGCAATCAGACAGTGGATATCTTC 60
QY 488 AGCAGTGTGAGACCAACATTTGAAACTCTTTGATGTCATGACTGTTGAGTGGGCC 547
|||||
Db 61 AGCAGTGTGAGACCAACATTTGAAACTCTTTGATGTCATGACTGTTGAGTGGGCC 120
QY 548 CCATATCAGGTGTGATTTCTTCACCTTCAGATGATGAGCAATGAGATGTTGAGGAA 607
|||||
Db 121 CCAATATCAGGTGTGATTTCTTCACCTTCAGATGATGAGCAATGAGATGTTGAGGAA 180
QY 608 GTGATGTGATCTTATGCAATGGAACACAGCTCTTCAGCATGTACAGCTATGAATG 667
|||||
Db 181 GTGATGTGATCTTATGCAATGGAACACAGCTCTTCAGCATGTACAGCTATGAATG 240
QY 668 AAGGCAATATGATATCATCAGCAATCATCTGTGCTGAAGCTAGCCAAAGGGGATAG 727
|||||
Db 241 AAGGCAATATGATATCATCAGCAATCATCTGTGCTGAAGCTAGCCAAAGGGGATAG 300
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|||||

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Db      301 GTTGGCTGCAATGGGCAATGGCGCTCTCCATGGGAGCCACCACCAAGCTTCTCCACCTTT 360
QY 788 GCAGGATTCCTGCTCTTTGAAACCTAAGTAATATATGACTAGATAGTACCTTGGGG 847
|||||
Db 361 GCAGGATTCCTGCTCTTTGAAACCTAAGTAATATATGACTAGATAGTACCTTGGGG 420
QY 848 AAGACTGTAGCTAGCGTGAATTTGTTACAGCTCAGGAACTTAAGTTGAGGTTTAC 907
|||||
Db 421 AAGACTGTAGCTAGCGTGAATTTGTTACAGCTCAGGAACTTAAGTTGAGGTTTAC 480
QY 908 ATTGCTGATTCACAAATATTTGTTGCAATCTTGTTCACAGCTACAGTACACCAATTA 967
|||||
Db 481 ATTGCTGATTCACAAATATTTGTTGCAATCTTGTTCACAGCTACAGTACACCAATTA 540
QY 968 TGTGGACAAATTCAGGGGCTCAGAGAATTCACCAACCAAAATAGTCTTCAGATGACCTT 1027
|||||
Db 541 TGTGGACAAATTCAGGGGCTCAGAGAATTCACCAACCAAAATAGTCTTCAGATGACCTT 600
QY 1028 GACTAATATATCTAGCATCTTATCAGCTCTTCTGGACCTTAAGATATATCTCTC 1087
|||||
Db 601 GACTAATATATCTAGCATCTTATCAGCTCTTCTGGACCTTAAGATATATCTCTC 660
QY 1088 TGACGACAGTTGGAATATTTTCTATCAGAACTATTCGAAATTTTGAATA 1147
|||||
Db 661 TGACGACAGTTGGAATATTTTCTATCAGAACTATTCGAAATTTTGAATA 717
QY 1148 CTCTGCTTTTAAATTTAAATACCAAGTTTTCAGGACC 1182
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Db 718 CTCTGCTTTT-ATTAAATACCAAGTTTTCAGGACC 751
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RESULT 5
BG400260
LOCUS   BG400260
DEFINITION BG400260 828 bp mRNA linear EST 12-MAR-2001
602464652F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592701 5',
mRNA sequence.
ACCESSION BG400260
VERSION   BG400260.1 GI:13293708
KEYWORDS EST.
SOURCE    human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS  National Institutes of Health, Mammalian Gene Collection (MGC)
1 (bases 1 to 828)
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
Email: rgabs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1331 row: h column: 14
High quality sequence stop: 740.
Location/Qualifiers
1. 828
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="IMAGE:4592701"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site: 1;
SfiI (ggcgctcgagc); Site: 2; SfiI (ggcgctcgagc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTAATGCTC-3' and 3' adaptor sequence:
5'-ATCTAGAGCCCGAGGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones

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Db 421 CAGCAGTGTGAGACCAACATTGGAACCTCTTGTGATGTCATGACTGGTAGATTGGGGC 480  
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Db 481 CCCAGTATCAGGCTGATGTTCTTCCACCTCGACATGATGAGCATGAGATGTTGAGGA 540  
OY 607 AGTGTATGTGATCCTTATGACATGGAACACAGCTCTTCCAGCATGATGATGATGAAT 666  
Db 541 AGTGTATGTGATCCTTATGACATGGAACACAGCTCTTCCAGCATGATGATGAAT 600  
OY 667 GAGGCGCAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 725  
Db 601 GAGGCGCAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
OY 726 AGCTTGGCTGGATGAGGCAATGAGGCTGCTGATGAGGCAACAGGCTTCTGACCT 785  
Db 661 GAGCTGTGCTGATGAGGCAATGAGGCTGCTGATGAGGCAACAGGCTTCTGACCT 718  
OY 786 TTGAGGATGCTGCTGCTTGAAGTAAATATATGATGATGATGATGATGATGATGATG 845  
Db 719 TTGAGGATGCTGCTGCTTGAAGTAAATATATGATGATGATGATGATGATGATG 777  
OY 846 GAGAGACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 884  
Db 778 GAGAGACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 814

## RESULT 7

LOCUS BG202940/c 840 bp mRNA linear EST 21-APR-2001  
DEFINITION RST22308 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
ACCESSION BG202940  
VERSION BG202940.1 GI:13724627  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 840)  
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.,  
Lerner,L., Costanzo,D., McElligott,K., Boozar,S., Mays,R., Smith,  
'E., Veloso,N., Kliska,A., Hess,J., Cothren,K., Lo,K., Offenbacher  
'J., Danzig,J., and Ducar,M.

TITLE Creation of genome-wide protein expression libraries using random

JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)

MEDLINE 21227151

COMMENT Contact: Scott J. Cain

Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: scaine@atersys.com

High quality sequence stop: 542.

## FEATURES

source

1. 840

/organism="Homo sapiens"

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/clone\_lib="Athersys RAGE Library"

/cell\_line="HT1080"

/note="See 'Creation of Genome-wide Protein Expression'

Libraries using Random Activation of Gene Expression',

Nature Biotechnology, in press. Note that even though the

cell type indicated is HT1080, since a random activation

method was used, these sequence tags are not necessarily

expressed in HT1080 under normal circumstances."

## BASE COUNT

256 a 154 c 161 g 268 t 1 others

## ORIGIN

Query Match 38.0%; Score 650; DB 12; Length 840;  
Best Local Similarity 97.2%; Pred. No. 2.8e-149;  
Matches 693; Conservative 0; Mismatches 16; Indels 4; Gaps 3;

OY 977 ATTGAGGGGCTCAGAGATCAACCAAAATAGCTTCTCAGATGACTGACTATAT 1036  
Db 718 AATTGGGGGCTCAGAGATCAACCAAAATAGCTTCTCAGATGACTGACTATAT 660  
OY 1037 ACTGAGCATCTTTATCTCTTCTTCCCTTGGACCTTAAAGATATCTCTGAGCAG 1096  
Db 659 ATACAGCATCTTTTACCTCTTCCCTTGGACCTTAAAGATATCTCTGAGCAG 601  
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OY 1157 TAAATTAATACAGTTTTCAGAGACCCCTGAGATTTTAACTTATCTTAAAT 1216  
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Db 480 TTGAGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 421  
OY 1277 CTTATTAATATTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1336  
Db 420 CTTATTAATATTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 361  
OY 1337 CCAGCAATATACATTTAAATCTGATGATGATGATGATGATGATGATGATGATG 1396  
Db 360 CCAGCAATATACATTTAAATCTGATGATGATGATGATGATGATGATGATGATG 303  
OY 1397 TAGCTATTAAGTGTGACCAAGTATGATGATGATGATGATGATGATGATGATG 1456  
Db 302 TAGCTATTAAGTGTGACCAAGTATGATGATGATGATGATGATGATGATGATG 243  
OY 1457 CCCCCAATCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1516  
Db 242 CCCCCAATCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 183  
OY 1517 ATCTCATGAGTACAGTGCACATGATGATGATGATGATGATGATGATGATGATG 1576  
Db 182 ATCTCATGAGTACAGTGCACATGATGATGATGATGATGATGATGATGATGATG 123  
OY 1577 TATATCTGAGAGCAATACATGATGATGATGATGATGATGATGATGATGATG 1636  
Db 122 TATATCTGAGAGCAATACATGATGATGATGATGATGATGATGATGATGATG 63  
OY 1637 AGATTAACCTGTGGCAAGAAAATGATGATGATGATGATGATGATGATGATGATG 1689  
Db 62 AGATTAACCTGTGGCAAGAAAATGATGATGATGATGATGATGATGATGATGATG 10

## RESULT 8

LOCUS BG204962

DEFINITION RST24381 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION BG204962

VERSION BG204962.1 GI:13726649

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 773)

AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.,  
Lerner,L., Costanzo,D., McElligott,K., Boozar,S., Mays,R., Smith,  
'E., Veloso,N., Kliska,A., Hess,J., Cothren,K., Lo,K., Offenbacher  
'J., Danzig,J., and Ducar,M.

TITLE Creation of genome-wide protein expression libraries using random

JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)

MEDLINE 21227151

COMMENT Contact: Scott J. Cain

Athersys, Inc.



3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scai@ethersys.com  
High quality sequence stop: 398.

## FEATURES

## SOURCE

1. 773  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Athersys RAGE Library"  
/cell\_line="HT1080"

/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 218 a 150 c 171 g 234 t  
ORIGIN

Query Match 37.4%; Score 639.8; DB 12; Length 773;

Best Local Similarity 94.7%; Pred. No. 9e-147; Mismatches 32; Indels 8; Gaps 5;

Matches 717; Conservative 0;

OY 428 ATTGATTCATGCTCTCTGCGAACCCACTTCAGCAATCAGAAAGAGGATTATCTTC 487  
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DB 1 ATTGATTCATGCTCTCTCTGCGAACCCACTTCAGCAATCAGAAAGAGGATTATCTTC 60  
OY 488 AGCACTGTTGAGACCAACATTGGAACCTTGTGATGTCATGCTGATGATTTGGGCC 547  
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DB 61 ACAGAGCTTGAGACCAACATTGGAACCTTGTGATGTCATGCTGATGATTTGGGCC 120  
OY 548 CCAGATTCAGGCTGATTTCTTACCTTCAGCATGATGAAGCATGATGATTTGAGGA 607  
|||||  
DB 121 CCAGATTCAGGCTGATTTCTTACCTTCAGCATGATGAAGCATGATGATTTGAGGA 180  
OY 608 GTGATGTTGATCTTATGCAATGAGCAACAGCTTCAGCATGATGAAGCATGATG 667  
|||||  
DB 181 GTGATGTTGATCTTATGCAATGAGCAACAGCTTCAGCATGATGAAGCATGATG 240  
OY 668 AAGGCAATTCAGATTCATGCAACATCATGCTGCTGCAAGCTTACGCAAGGAGATG 727  
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DB 241 AAGGCAATTCAGATTCATGCAACATCATGCTGCTGCAAGCTTACGCAAGGAGATG 300  
OY 728 GTTGGCTGCGATGCGCAATGCGCTGCTCCATGCGGACACCAAGCTTCCACCTT 787  
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DB 301 GTTGGCTGCGATGCGCAATGCGCTGCTCCATGCGGACACCAAGCTTCCACCTT 360  
OY 788 GCAGATTCCTGCTCTTGAACATGATTAATATGATGATGATGATGATGATGATG 847  
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DB 361 GCAGATTCCTGCTCTTGAACATGATTAATATGATGATGATGATGATGATGATG 420  
OY 848 AAGACTTGTAGCTGAGCTGATTTGTAGCATGAGCAACATTAAAGTTGAGGTTTAC 907  
|||||  
DB 421 AAGACTTGTAGCTGAGCTGATTTGTAGCATGAGCAACATTAAAGTTGAGGTTTAC 480  
OY 908 ATTGCTGATTCAGAAATATGTTGCAATGTTGCAATGTTGCAATGTTGCAATG 967  
|||||  
DB 481 ATTGCTGATTCAGAAATATGTTGCAATGTTGCAATGTTGCAATGTTGCAATG 540  
OY 968 TG-TTGGAATATCAGGGGCTCAGAGAAATCAACCAAAAT-AGTCTTTCAGATGAC 1025  
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DB 541 TGTTTGAGACATTCAGGGGCTCAGAGAAATCAACCAAAATAGCTTTCAGATGAC 600  
OY 1026 TTGACTAATATATCAGCATCTTTATCAGCTCTTGGACCTTAAGATATCTCC 1085  
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DB 601 TTGACTAATATATCAGCATCTTTATCAGCTCTTGGACCTTAAGATATCTCC 658  
OY 1086 TGTGAGAGAGTTGGAATATTTTCTATCAGAGAGATGATGATGATGATGATGATG 1145  
|||||  
DB 659 TGTGAGAGAGTTGGAAT-ATTTTATTTATTAATCAGAGAGATGATGATGATGATG 716  
OY 1146 TACTCTGCTTTAATTAATTAATCAGATTTTCAGAGAAC 1182

DB 717 GGTTCG-TTTAAATTAATACAGGCTTAAGAACCC 751

## RESULT 9

## LOCUS

## DEFINITION

B0637986 636 bp mRNA linear EST 15-JUL-2002  
hd17a10.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he

Hom sapiens cDNA clone hd17a10 5', mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graham@helix.nih.gov  
Plate: 17 row: a column: 10  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
1. 636  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="hd17a10"  
/clone\_lib="Human Retina cDNA (Un-normalized, unamplified)"  
): hd/he"  
/tissue\_type="Retina"  
/dev\_stage="Adult"  
/lab\_host="EMD108"  
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor (5'-pGACTGTGTTTAAATGCGGCGGCCGCC(7)15-3'. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

## FEATURES

## SOURCE

BASE COUNT 155 a 156 c 177 g 148 t  
ORIGIN

Query Match 36.5%; Score 625; DB 14; Length 636;

Best Local Similarity 100.0%; Pred. No. 3.9e-143; Mismatches 0; Indels 0; Gaps 0;

Matches 625; Conservative 0;

OY 20 CAGGCTCCGAGCTCTGCTGCTTCTCAGGAGACTGAGGCTGTTGAGAAATCATG 79  
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DB 12 CAGGCTCCGAGCTCTGCTGCTTCTCAGGAGACTGAGGCTGTTGAGAAATCATG 71  
OY 80 CTTTGAGAGAGCTCATCTATTTGCAACTGCTGGCTTTGTTTCTCCCTTTTGGCTG 139  
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DB 72 CTTTGAGAGAGCTCATCTATTTGCAACTGCTGGCTTTGTTTCTCCCTTTTGGCTG 131  
OY 140 TGTCAAGATGAATATGAGCTCTCCACAAACCGAGAGATACCCGACGACTGAGTAAG 199  
|||||  
DB 132 TGTCAAGATGAATATGAGCTCTCCACAAACCGAGAGATACCCGACGACTGAGTAAG 191





[illegible]

| QY                    | 1551  | ATGTTGCACTGTGACACCAAGGAGTTTATATCTGGAAGAACATACCTTTATATTAATACC | 1610               |
|-----------------------|---|--|--------------------|
| Db                    | 149   | ATGTTGCACTGTGACACCAAGGAGTTTATATCTGGAAGAACATACCTTTATATTAATACC | 90                 |
| QY                    | 1611  | TTAGAGAAAGATTTTGACCTGCTTATAGATAAACTGTGCGAAGAAAATGTAAATGACCA  | 1670               |
| Db                    | 89  | TTAGAGAAAGATTTTGACCTGCTTATAGATAAACTGTGCGAAGAAAATGTAAATGACCA  | 30                 |
| QY                    | 1671  | ATATATGGAATTA 1684   |                    |
| Db                    | 29  | CATTAGCAAAATTA 16  |                    |
| RESULT 12             |   |  |                    |
| BM819819              |   | 600 bp   | linear             |
| LOCUS                 |   |  |                    |
| DEFINITION            | K-EST0088027 S18N669761 Homo sapiens CDNA clone S18N669761-17-A08   |  |                    |
| ACCESSION             | BM819819  |  |                    |
| VERSION               | BM819819.1  | GI:19176232  |                    |
| KEYWORDS              | EST.  |  |                    |
| SOURCE                | human.  |  |                    |
| ORGANISM              | Homo sapiens  |  |                    |
| REFERENCE             | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.   |  |                    |
| AUTHORS               | 1 (bases 1 to 600)<br>Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.   |  |                    |
| TITLE                 | 21C Frontier Korean EST Project 2001  |  |                    |
| JOURNAL               | Unpublished (2002)  |  |                    |
| COMMENT               | Contact: Kim YS<br>Genome Research Center<br>Korea Research Institute of Bioscience & Biotechnology<br>52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea<br>Tel: +82-42-860-4470<br>Fax: +82-42-860-4409<br>Email: yongsung@email.kribd.re.kr<br>Plate: 17 row: A column: 08<br>High quality sequence stop: 600.   |  |                    |
| FEATURES              |   |  |                    |
| Source                | Location/Qualifiers   |  |                    |
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|                       | /organism="Homo sapiens"  |  |                    |
|                       | /db_xref="taxon:9606"   |  |                    |
|                       | /clone="S18N669761-17-A08"  |  |                    |
|                       | /clone_lib="S18N669761"   |  |                    |
|                       | /sex="F"  |  |                    |
|                       | /lab_host="Top10F"  |  |                    |
|                       | /note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI, Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adistised to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library." |  |                    |
| BASE COUNT            | 174 a 118 c 105 g 203 t   |  |                    |
| ORIGIN                |   |  |                    |
| Query Match           | 35.0%;  | Score 599;   | DB 14; Length 600; |
| Best Local Similarity | 100.0%;   | Pred. No. 9,8e-137;  |                    |
| Matches 599;          | Conservative 0;   | Mismatches 0;  | Indels 0; Gaps 0;  |





plasmid DNA was mixed with 5 micrograms PCR product  
representing library inserts and hybridized to an EcoI of  
20. Single-stranded (unhybridized) plasmids were isolated  
by hydroxyapatite chromatography and used to make this  
library.

BASE COUNT 165 a 109 c 122 g 159 t  
ORIGIN

Query Match 32.4%: Score 555; DB 13; Length 555;

Best Local Similarity 100.0%; Pred. No. 6.7e-126;

Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 582 TGATGAAGCATGAGAGATGTTGAGAGATGATGTGACCTTATGCACATGCAACACAG 641  
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Db 1 TGATGAAGCATGAGAGATGTTGAGAGATGATGTGACCTTATGCACATGCAACACAG 60  
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OY 642 TCTTCAGCATGTACAGCTATGAAATGAAGGCAATCAGATACATCCAGCATCATGCTG 701  
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Db 61 TCTTCAGCATGTACAGCTATGAAATGAAGGCAATCAGATACATCCAGCATCATGCTG 120  
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OY 702 TGCCTGAAGCTGACCAAGAGGATGAGTTTGGCTGCGAATGGCAATGGCGCTCTCCATG 761  
|||  
Db 121 TGCCTGAAGCTGACCAAGAGGATGAGTTTGGCTGCGAATGGCAATGGCGCTCTCCATG 180  
|||  
OY 762 GGGACCAACACGCTTCTCCACCTTTGCGAGATTCCTGCTTTGAACCTAAGTAAATAT 821  
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Db 181 GGGACCAACACGCTTCTCCACCTTTGCGAGATTCCTGCTTTGAACCTAAGTAAATAT 240  
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OY 822 ATGACTAGAAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGATCG 881  
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Db 241 ATGACTAGAAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGATCG 300  
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OY 882 AGGAACATTAAGTTGAGGGTTTACATGCTGTATTCAAAATATATGTTGCTGCAATGT 941  
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Db 301 AGGAACATTAAGTTGAGGGTTTACATGCTGTATTCAAAATATATGTTGCTGCAATGT 360  
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OY 942 TGTTCACGCTACAGGTACCAATATGTTGACAAATTGAGGGCTCAGAGAATCAACC 1001  
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Db 361 TGTTCACGCTACAGGTACCAATATGTTGACAAATTGAGGGCTCAGAGAATCAACC 420  
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OY 1002 ACAAAATAGTCTTCAGATGACCTTGACTAATATACTCAGCATCTTATCAGCTTTCC 1061  
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Db 421 ACAAAATAGTCTTCAGATGACCTTGACTAATATACTCAGCATCTTATCAGCTTTCC 480  
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OY 1062 TTGCACCTAAAGATATTTCTCTGACGACAGTTGGAATATTTTTCATACAG 1121  
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Db 481 TTGCACCTAAAGATATTTCTCTGACGACAGTTGGAATATTTTTCATACAG 540  
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OY 1122 AAGTCATTTGCAAG 1136  
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Db 541 AAGTCATTTGCAAG 555  
|||

Search completed: January 15, 2003, 19:31:52  
Job time : 2259 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 15, 2003, 17:17:45 : Search time 83 Seconds

(without alignments)  
6325.670 Million cell updates/sec

Title: US-10-036-041-1

Perfect score: 1712

Sequence: 1 ggcacatgcggcggagagacc.....ttgttaagaataaaaaa 1712

Scoring table: IDENTITY\_MUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Issued\_Patents\_NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PTC05.COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/Backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 696.2 | 40.7        | 1123   | 3     | US-09-188-930-28   |
| 2          | 696.2 | 40.7        | 1123   | 3     | US-09-188-930-203  |
| 3          | 78.8  | 4.6         | 3375   | 4     | US-09-370-838-151  |
| 4          | 74.6  | 4.4         | 1313   | 2     | US-08-463-911-6    |
| 5          | 74.6  | 4.4         | 4517   | 4     | US-09-140-804-9    |
| 6          | 72.8  | 4.3         | 1868   | 1     | US-08-392-367B-1   |
| 7          | 72.8  | 4.3         | 1868   | 1     | US-08-893-467A-1   |
| 8          | 70.4  | 4.1         | 1276   | 2     | US-08-463-911-1    |
| 9          | 68    | 4.0         | 1560   | 2     | US-08-794-795-5    |
| 10         | 68    | 4.0         | 1560   | 4     | US-09-249-200-5    |
| 11         | 66.4  | 3.9         | 1703   | 2     | US-08-794-795-1    |
| 12         | 66.4  | 3.9         | 1703   | 4     | US-09-249-200-1    |
| 13         | 63.6  | 3.7         | 729    | 4     | US-09-140-804-10   |
| 14         | 61.8  | 3.6         | 750    | 3     | US-09-188-930-19   |
| 15         | 61.8  | 3.6         | 1107   | 3     | US-09-188-930-217  |
| 16         | 60.2  | 3.5         | 1560   | 4     | US-09-453-702B-264 |
| 17         | 60.2  | 3.5         | 61663  | 4     | US-09-453-702B-62  |
| 18         | 59    | 3.4         | 1341   | 2     | US-08-945-848-7    |
| 19         | 59    | 3.4         | 2363   | 2     | US-08-945-848-6    |
| 20         | 58    | 3.4         | 5102   | 1     | US-08-494-168-1    |
| 21         | 57.2  | 3.3         | 1572   | 4     | US-09-297-269-39   |
| 22         | 56.6  | 3.3         | 653    | 4     | US-09-336-536-32   |
| 23         | 56.6  | 3.3         | 843    | 4     | US-09-118-408-23   |
| 24         | 56.6  | 3.3         | 843    | 4     | US-09-506-855-23   |
| 25         | 56.4  | 3.3         | 3181   | 1     | US-08-655-086-1    |
| 26         | 55.8  | 3.3         | 1839   | 1     | US-08-383-744-1    |
| 27         | 55.8  | 3.3         | 1839   | 2     | US-08-999-336-1    |

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|----|------|-----|-------|---|--------------------|-------------------|
| 28 | 55.8 | 3.3 | 1839  | 5 | PCT-US96-01427-1   | Sequence 1, Appl  |
| 29 | 55.6 | 3.2 | 4359  | 4 | US-09-484-970B-4   | Sequence 4, Appl  |
| 30 | 54.2 | 3.2 | 392   | 4 | US-09-404-879A-372 | Sequence 372, App |
| 31 | 54.2 | 3.2 | 1333  | 4 | US-09-227-357-51   | Sequence 51, App  |
| 32 | 53.2 | 3.1 | 324   | 4 | US-09-404-879A-290 | Sequence 290, App |
| 33 | 53   | 3.1 | 1416  | 2 | US-07-621-091G-1   | Sequence 1, Appl  |
| 34 | 53   | 3.1 | 1416  | 2 | US-08-399-889-1    | Sequence 1, Appl  |
| 35 | 53   | 3.1 | 1416  | 3 | US-09-167-364-1    | Sequence 1, Appl  |
| 36 | 53   | 3.1 | 1416  | 4 | US-09-439-897-1    | Sequence 1, Appl  |
| 37 | 51.8 | 3.0 | 2543  | 1 | US-08-555-666-11   | Sequence 11, Appl |
| 38 | 51.8 | 3.0 | 2543  | 3 | US-09-073-663-11   | Sequence 11, Appl |
| 39 | 51.2 | 3.0 | 38584 | 4 | US-09-453-702B-50  | Sequence 50, Appl |
| 40 | 51   | 3.0 | 444   | 4 | US-09-397-787-161  | Sequence 161, App |
| 41 | 50.6 | 3.0 | 4031  | 1 | US-08-159-784-1    | Sequence 1, Appl  |
| 42 | 50.2 | 2.9 | 9827  | 4 | US-09-453-702B-66  | Sequence 66, Appl |
| 43 | 49.8 | 2.9 | 9827  | 4 | US-09-247-155-153  | Sequence 153, App |
| 44 | 49.2 | 2.9 | 1347  | 4 | US-09-140-804-1    | Sequence 1, Appl  |
| 45 | 48.8 | 2.9 | 1608  | 4 | US-09-029-348-19   | Sequence 19, Appl |

## ALIGNMENTS

|  |     |   |     |  |  |  |  |  |  |
|--|-----|---|-----|--|--|--|--|--|--|
| RESULT 1   |     |   |     |  |  |  |  |  |  |
| US-09-188-930-28   |     |   |     |  |  |  |  |  |  |
| : Sequence 28, Application US/09188930A                        |     |   |     |  |  |  |  |  |  |
| : Patent No. 6150502   |     |   |     |  |  |  |  |  |  |
| : GENERAL INFORMATION:   |     |   |     |  |  |  |  |  |  |
| : APPLICANT: Watson, James D.                                  |     |   |     |  |  |  |  |  |  |
| : APPLICANT: Strachan, Lorna                                   |     |   |     |  |  |  |  |  |  |
| : APPLICANT: Sleeman, Matthew                                  |     |   |     |  |  |  |  |  |  |
| : APPLICANT: Onrust, Rene                                      |     |   |     |  |  |  |  |  |  |
| : TITLE OF INVENTION: Compositions Isolated From Skin Cells    |     |   |     |  |  |  |  |  |  |
| : FILE OF INVENTION: and Methods For Their Use                 |     |   |     |  |  |  |  |  |  |
| : FILE REFERENCE: 11000.1011c1                                 |     |   |     |  |  |  |  |  |  |
| : CURRENT APPLICATION NUMBER: US/09/188,930A                   |     |   |     |  |  |  |  |  |  |
| : NUMBER OF SEQ ID NOS: 348                                    |     |   |     |  |  |  |  |  |  |
| : SOFTWARE: FastSeq for Windows Version 3.0                    |     |   |     |  |  |  |  |  |  |
| : SEQ ID NO: 28  |     |   |     |  |  |  |  |  |  |
| : LENGTH: 1123   |     |   |     |  |  |  |  |  |  |
| : TYPE: DNA  |     |   |     |  |  |  |  |  |  |
| : ORGANISM: Rat  |     |   |     |  |  |  |  |  |  |
| US-09-188-930-28   |     |   |     |  |  |  |  |  |  |
| Query Match  |     |   |     |  |  |  |  |  |  |
| Best Local Similarity 40.7%; Score 696.2; DB 3; Length 1123;   |     |   |     |  |  |  |  |  |  |
| Matches 819; Conservative 0; Mismatches 168; Indels 2; Gaps 2; |     |   |     |  |  |  |  |  |  |
| QY   | 33  | CTCTGCTGCTCTTCAAGGAGACTGTGAGGCTGTGTGAGAAATCATGCTTTGGAGGCAGC | 92  |  |  |  |  |  |  |
| DB   | 136 | CCCATGAGTCTCCCGGCGAGATTCGCCATTTGTCACAGGCATGCTCAGAGGCAGC     | 195 |  |  |  |  |  |  |
| QY   | 93  | TCATCTATTGGCAAGTGGCTGTTGTTTCCCTTTTGGCTGCTGTGCAAGATGAAT      | 152 |  |  |  |  |  |  |
| DB   | 196 | TCGTCTGGTGGCACTGCTGCTGCTTTTCTCCATTTTGTGCTGTGCAAGATGAAT      | 255 |  |  |  |  |  |  |
| QY   | 153 | ACATGAGTCTCCCAACCGAGAGACTATCCCAAGCTGCAAGTGAATGTTGTATGAG     | 212 |  |  |  |  |  |  |
| DB   | 256 | ACATGAGTCTCCCAACCGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG     | 315 |  |  |  |  |  |  |
| QY   | 213 | ACTACAGCTTTGAGGCTACCAAGGCCCCCTGGGCCACGGGCTCTGCGATTCCAG      | 272 |  |  |  |  |  |  |
| DB   | 316 | ATTATGATTCCCTGTTTACCAAGGCGCCCTGAGCCCTCCAGGTCTCTGCGATTCCAG   | 375 |  |  |  |  |  |  |
| QY   | 273 | GAAACCATGGAACATGCAATGCAAGCCACTGGTCTGTAAGGAGCAAGAGTGAGA      | 332 |  |  |  |  |  |  |
| DB   | 376 | GAAACCATGGAACATGCAATGCAAGCCACTGGCCCGAAGGAGGCAAGGAGTGA       | 435 |  |  |  |  |  |  |
| QY   | 333 | AGGCGCACAAGGTGAGCTGGGCTCTGAGGGAGGCGGGGAGCATGAGCCCAAGAG      | 392 |  |  |  |  |  |  |
| DB   | 436 | AAGGAGCAAAAGCGACCTGGGCTCTGAGGGAGCAAGCGGGGAGCATGAGCCCAAGAG   | 495 |  |  |  |  |  |  |





|                           |       |                   |          |             |
|---------------------------|-------|-------------------|----------|-------------|
| Query Match               | 4.6%  | Score 78.8        | DB 4     | Length 3275 |
| Best Local Similarity     | 52.4% | Pred. No. 5.2e-13 |          |             |
| Matches 173; Conservative | 0     | Mismatches 157    | Indels 0 | Gaps 0      |

RESULT 4  
US-08-463-911-6

1 APPLICANT: Scherer, Philipp E.  
2 APPLICANT: Loidish, Harvey F.  
3 TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED  
4 TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES  
5 NUMBER OF SEQUENCES: 7  
6 CORRESPONDENCE ADDRESS:  
7 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
8 STREET: Two Midlila Drive  
9 CITY: Lexington  
10 STATE: Massachusetts  
11 COUNTRY: USA  
12 ZIP: 02173  
13  
14 COMPUTER READABLE FORM:  
15 MEDIUM TYPE: Floppy disk  
16 COMPUTER: IBM PC compatible  
17 OPERATING SYSTEM: PC-DOS/MS-DOS  
18 SOFTWARE: PatentIn Release #1.0, Version #1.30  
19 CURRENT APPLICATION DATA:  
20 APPLICATION NUMBER: US/08/463,911

|                       |                 |                    |           |              |
|-----------------------|-----------------|--------------------|-----------|--------------|
| Query Match           | 4.4%;           | Score 74.6;        | DB 2;     | Length 1313; |
| Best Local Similarity | 50.4%;          | Pred. No. 5.4e-12; |           |              |
| Matches 210;          | Conservative 0; | Mismatches 204;    | Indels 3; | Gaps 1;      |

|    |     |  |     |
|----|-----|--|-----|
| Oy | 219 | GCTTTCAGGCTTACCAAGGCCCCCTCGGCGACGCGGCCCTCTCGGATTCACAGGAACC     | 278 |
| Db | 197 | GCATCCCAAGGCATCCGGGCCATATATGGGGCCCAAGGCCGTGATGGCAGAGATGGCACCC  | 256 |
| Oy | 279 | ATGGAACAATGGCAACAAATGGAGCCACTGTCATGAAGAGCCAAAGGTGAGAAAGGCC     | 338 |
| Db | 257 | CTGGAGAAAGGCTGAGAAAGAGATCCAGGTCTTATTGGTCTTAAGGGAGACATCGGTG     | 316 |
| Oy | 339 | ACAAAGGTGACCTTGGGCTTCGAGGGGACGGGGGGGAGCATATGGCCCCAAAGAGAGAAAG  | 398 |
| Db | 317 | AAACCGGGATCCCGGGGCTGAAGGTCGCCGAGGCTTTCGGGGAATCCAAGGACGAAG      | 376 |
| Oy | 399 | GCTACCCGGG---GATTCCACACCAACTTACAGATTGCATTCAGGCTCTCTGGCAACC     | 455 |
| Db | 377 | GAGAACCTGGGAAGGTGCTCATGTATATACCCGTACAGATTACGTGTGGATTGGAAGCTT   | 436 |
| Oy | 456 | ACTTCAGCAATCAGACACAGTGGGATTATCTTCAGCAGCTGTTGAGAACCAACATTGGAACT | 515 |
| Db | 437 | ACGTTACTATCCCAACATGCGCCATTCGCTTACCAGAGATCTTACAAACACGACAAACC    | 496 |
| Oy | 516 | TCTTTGATGTATACGTGTGTAGATTGTGGGCCCCAGATATCAGTGTATTTCCTTCAACT    | 575 |
| Db | 497 | ACTATGATGGCTCCACGTGTAAATTCACATGCAACATTCCTCGGGCTGTACTACTTCCCT   | 556 |
| Oy | 576 | TCACATGATATCAACATGAGAGATGTTGAGCAAGGTATATGTACTTATTCACATG        | 632 |
| Db | 557 | ACCAATATCAGCTTATATGTAGAAGATGTGAAGGTCCAGCCTTCTTACAGAGACACAGG    | 613 |

```

; RESULT 5
; US-09-140-804-9
; Sequence 9, Application US/09140804
; Patent No. 6197910
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 4517
; TYPE: DNA
; ORGANISM: Homo sapiens

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1 REFERENCE/DOCKET NUMBER: TRV 2 009
2
3 TELECOMMUNICATION INFORMATION:
4
5 TELEPHONE: (216) 861-5582
6
7 TELEFAX: (216) 241-1666
8
9 TELEX: (216) 980162
10
11 INFORMATION FOR SEQ. ID NO: 1:
12
13 SEQUENCE CHARACTERISTICS:
14
15 LENGTH: 1866 base pairs
16
17 TYPE: Nucleic acid
18
19 STRANDEDNESS: Single
20
21 TOPOLOGY: Linear
22
23 MOLECULE TYPE: Nucleotide-genomic DNA
24
25 HYPOTHEICAL: No. 6063901 relevant
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27 ANTI-SENSE: No. 6063901 relevant
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|                           |       |                   |           |             |
|---------------------------|-------|-------------------|-----------|-------------|
| Query Match               | 4.3%  | Score 72.8        | DB 3      | Length 1868 |
| Best Local Similarity     | 58.2% | Pred. No. 2.2e-11 |           |             |
| Matches 128; Conservative | 0;    | Mismatches 92;    | Indels 0; | Gaps 0      |

|    |     |  |      |
|----|-----|--|------|
| Qy | 201 | GTTTCATCATGAGACTATACAGCTTTCGAGGATACCAAGGCCCCCTGGGGCCACGCGGGCCCTC | 2670 |
| Db | 707 | GTCGTGATGGGAACCCCAAGGTGTCCAAAGACCCCAAGGCGCCACAGGATGCAAGAGAGAGG   | 7666 |
| Qy | 261 | CTGGCATTCACGGAACCATATGGAAACAAATGGACGCCTGTCATGAAGGAG              | 3202 |
| Db | 767 | CAGGCTCTCAGAGGACTTACGGGTGCACACGAGGAAGCAAGGAGCACTGTGTCTCCAGGAC    | 8236 |
| Qy | 321 | CCAAAGTGAGAGAGGCGCACAAAGTGCCTGGGGCTCGAAGGGGAGCGGGGGCAGCATG       | 3808 |
| Db | 827 | CTCAGAGGAGAAAGGCGCAGCAAAAGTGACATAGGTCTCACCTGGGCCCCAAGGGGGACATG   | 8866 |
| Qy | 381 | GCCCCAAAGGAGAGAGGGCTACCCGGGGATTCCACACAGA                         | 420  |
| Db | 887 | GCACCAAGGGAGACAAAGGGGACTACGCGCTTCACGAGAAA                        | 926  |

RESULT 8  
US-08-463-911-1  
Sequence 1, Application US/08463911  
Patent No. 5869330  
GENERAL INFORMATION:  
APPLICANT: Scherer, Phillip E.  
APPLICANT: Lodish, Harvey E.  
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED  
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millita Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: -02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,911  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: WH195-05  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ. ID NO.: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1276 base pairs

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..786
;
US-08-463-911-1

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|                       |              |                   |                |             |
|-----------------------|--------------|-------------------|----------------|-------------|
| Query Match           | 4.1%         | Score 70.4        | DB 2           | Length 1276 |
| Best Local Similarity | 48.7%        | Pred. No. 9.2e-11 |                |             |
| Matches 222           | Conservative | 0                 | Mismatches 231 | Indels 3    |
|                       |              |                   |                | Gaps 1      |

|    |     |  |     |
|----|-----|--|-----|
| QY | 219 | GCCTTCAGGCTTACCAAGCCCCCTGGGACCCGGGCCCCCTCCGGCATTTCCAGGAAAC       | 278 |
| Db | 179 | GCATCCCAAGACATCTGGCTCCACATGGACACCCAGGCCCGATGGCAGATGGCACTC        | 238 |
| QY | 279 | ATGGAACAATGGCCACACATGTGAGACCCTACTGTCTATGAAAGAGCCAAAGTGTGAGAGGGC  | 338 |
| Db | 239 | CTGGAGAACAAAGGAGAAAGAAATGCAGATGCAGATCTCTTTGGTCCCTAAAGGTGAGACAGAG | 298 |
| QY | 339 | ACAAAGGTGACCTGGGGCTTCGAGGGGAGCGGGGGGCAAGCATGCCCCCAAGAGAGAAAG     | 398 |
| Db | 299 | ATGTGGTAATACACAGGAGCTGAAAGGGCAGCGGGCTTCCCGGAACCCCTGGAGAGAAAG     | 358 |
| QY | 399 | GCTACCCGGGATTTCCACACAACT---TCGATTTGCATTCATGCTTCTCTGGCAACC        | 455 |
| Db | 359 | GAGAGCCTCGAGAAACCCGCTTATTTGATTCGCTCAGCGCTTCAGTGTGGGCTGGAGACC     | 418 |
| QY | 456 | ACTTCAGCAATCACAAACAGTGGATTATCTTCAGCAGCTGTTGAGACCACAACTTGGAACT    | 515 |
| Db | 419 | GGGTCACTGTTCCCAATGTATCCCAATTTGGCTTCTACTAAGATCTCTACAAACCAACAGATC  | 478 |
| QY | 516 | TCTTTGATGTATCACTGCTGTGATTTGGGGCCCAAGATCAGGTGTGTATTTCTGCCT        | 575 |
| Db | 479 | ATTATGAGCGGACGACTGGCAAGTTCTACTACGTCAACATTCGGGGCTCTACTACTTCTT     | 538 |
| QY | 576 | TCAGCATCATCAAGCATGAGAGATTGGAGAAGTGTATGTGTACTTATGCACATGGCA        | 635 |
| Db | 539 | ACCACATCAAGGTTATCATGAAAGATGTGAAGGTGAGAGCTTCTCAAGAGACAAAGCCG      | 598 |
| QY | 636 | ACACAGCTTTCAGCATGTACAGCTATGAAATGAAG                              | 671 |
| Db | 599 | TTCTCTTCACTACCAACCATATGAGGAAAGATG                                | 634 |

RESULT 9  
 ; Sequence 5, Application US/08794795  
 ; Patent No. 5916766  
 GENERAL INFORMATION:  
 APPLICANT: Elshouriaqy, Nabil  
 APPLICANT: Adamou, John  
 APPLICANT: Gross, Mitchell  
 APPLICANT: Lysko, Paul  
 TITLE OF INVENTION: Human Macro Scavenger Rec  
 TITLE OF INVENTION: eplor  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Smithsonian Beecham Corporation  
 STREET: 709 Swedeland Road  
 CITY: King of Prussia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19406  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSED for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/794,795  
 FILING DATE: 04-FEB-1997





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us-10-036-041-1.rni

Page 8

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Db      292  TGWWSNGTNCNCNMGNMNSNGCNTTYWWSNGCNAARMGMNSNMNGNTNCCNCCN 351
Oy      464  AATCAGAACAGTGGGGATTATCTTCACGACATGTTGAGAACCAACATTTGGAACTCTTGAT 523
Db      352  CCNWSNGATGCMCCNTTNCNCNTTYGAYMGNWTYNTGTNAAGARCARCGNCAYTAYGAV 411
Oy      534  GTCATGACTGTAGATTTGGGGCCCCAGATGATGAGGTGTATTTCTTCACTTCACACATG 583
Db      412  GCGNTNACGNGAARATTTACNTGYCARGTNCCNGSGNTATATATYTTTCGNGNCAYGCA 471
Oy      584  ATGAAGCATGAGAGATGTTGAGCAAGTGTATGTGTACTTATGCACACATGGCAACACATC 643
Db      472  ACNGTNTATYMGNCWMSNTYTNCARTTYGAYYT---NGTNAARAAYGNGNARWMSNATHGCA 528
Oy      644  TTCACCATGTATGAGTATGAAATGAAGGCCAATCGATACATCCAGCATATGCTGTG 703
Db      529  WSNITTYTTCATTTTYYTGNGNGNTGGCCNAARCCGCMWSNTYTNNSGNGSGNCGNATG 588
Oy      704  CTGAAGCTAGCCAAAGGGGATGAGTTTGGCTGCGAATGGGCAATGGCCCTCTCCATGG 763
Db      589  GTNMGNNTTGARCCNGARGAYCARGTNTGGGTNCACGTGNGGNTGNGNCAATYATATHGN 648
Oy      764  GACCAACCAACGCTTCTCCACCTTTGCAGAGATTCTGCTCTTT 805
Db      649  ATHTAYGCNWSNATHARACNGAYWSNACNTTYWSNGNTTY 690

RESULT 14
US-09-188-930-19
; Sequence 19, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Muirson, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Rat
US-09-188-930-19

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US-09-188-930-217.
: Sequence 217, Application US/09188930A
: Patent No. 6150502
: GENERAL INFORMATION:
: APPLICANT: Watson, James D.
: APPLICANT: Strachan, Lorna
: APPLICANT: Sleeman, Matthew
: APPLICANT: Onrust, Rene
: APPLICANT: Murison, James Greg
: TITLE OF INVENTION: Compositions Isolated From Skin Cells
: TITLE OF INVENTION: and Methods For Their Use
: FILE REFERENCE: 11000.1011c1
: CURRENT APPLICATION NUMBER: US/09/188,930A
: CURRENT FILING DATE: 1998-11-09
: NUMBER OF SEQ ID NOS: 348
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 217
: LENGTH: 1107
: TYPE: DNA
: ORGANISM: Rat
US-09-188-930-217

Query Match          3.6%; Score 61.8; DB 3; Length 1107;
Best Local Similarity 56.0%; Pred: No. 2.9e-08;
Matches 117; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

0Y 207 ATGGAAGACTACAGCTTTGAGAGCTTCAAGCCGCCCCCTGGGGCACCAGGGCCCTCCTGGCA 266
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 379 ACGGCCAGGACGCGAACCAGAGGGGACAGTGGGAGAAAGAGTCCCTCCTGGCAGACAGCA 438
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0Y 267 TTCGAGGAATCCATGAAACAATGGCAACATGAGCCACTGGTCATGAGAGGCCAAAG 326
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 439 ACCGGAGAGAAACACAAAGGACCAAGGGCAGCTGGGCCATTGGAGAGCGGGTCTCCGAG 498
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0Y 327 GTGAAAGAGGGGCGACAAGAGTGACCTGGGGCCCTCGAAGGGAGGGGGGGCGCAGCATGGCCCCA 386
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 499 GACCCAGAGGGGGTCACTAGTGGTACCCCGGGGAAACATGTATTACCGGGCAAGAGGACCTTA 558
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0Y 387 AAGGAGAGAGAGGCTACCCGGGGATTTCA 415
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 559 AGGCGAAGAAAGGGGAGACCTGGGCTCCCA 587
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

Search completed: January 15, 2003, 19:33:31
Job time : 100 secs

```

## RESULT 15

[illegible]

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 15, 2003, 17:41:40 (Search time 79 Seconds  
(without alignments)  
414.932 Million cell updates/sec

Title: US-10-036-041-2

Perfect score: 1367

Sequence: 1 MLMROLIYQDLALFLPLPC.....LHGDHQRFSFACGLFETK 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: A\_Geneseq\_101002: \*  
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT: \*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT: \*  
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT: \*  
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT: \*  
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT: \*  
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT: \*  
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT: \*  
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT: \*  
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT: \*  
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT: \*  
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT: \*  
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT: \*  
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT: \*  
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT: \*  
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT: \*  
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT: \*  
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT: \*  
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT: \*  
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT: \*  
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT: \*  
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT: \*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------|
| 1          | 1367   | 100.0       | 246    | 21 | AA15548     |
| 2          | 1367   | 100.0       | 246    | 21 | AA15548     |
| 3          | 1367   | 100.0       | 246    | 21 | AA15548     |
| 4          | 1367   | 100.0       | 246    | 22 | AA18909     |
| 5          | 1367   | 100.0       | 246    | 22 | AA18909     |
| 6          | 1320.5 | 95.9        | 246    | 23 | AA18909     |
| 7          | 1311   | 95.9        | 246    | 23 | AA18909     |
| 8          | 1208   | 88.4        | 225    | 22 | AA18909     |
| 9          | 884    | 64.7        | 202    | 22 | AA18909     |
| 10         | 792.5  | 58.0        | 223    | 22 | AA18909     |

|    |       |      |     |    |         |
|----|-------|------|-----|----|---------|
| 11 | 721   | 52.7 | 128 | 20 | AA11485 |
| 12 | 663   | 48.5 | 126 | 22 | AA14074 |
| 13 | 582   | 42.6 | 105 | 21 | AA17599 |
| 14 | 582   | 42.6 | 105 | 21 | AA17602 |
| 15 | 582   | 42.6 | 105 | 22 | AA15590 |
| 16 | 582   | 42.6 | 105 | 22 | AA15596 |
| 17 | 582   | 42.6 | 105 | 23 | AA17210 |
| 18 | 582   | 42.6 | 105 | 23 | AA17216 |
| 19 | 325   | 23.8 | 267 | 23 | AA18437 |
| 20 | 319   | 23.3 | 285 | 21 | AA17610 |
| 21 | 319   | 23.3 | 285 | 22 | AA15604 |
| 22 | 319   | 23.3 | 285 | 23 | AA17224 |
| 23 | 316   | 23.1 | 294 | 21 | AA17603 |
| 24 | 316   | 23.1 | 294 | 22 | AA15597 |
| 25 | 316   | 23.1 | 294 | 23 | AA17217 |
| 26 | 315.5 | 23.1 | 288 | 22 | AA15644 |
| 27 | 315   | 23.0 | 289 | 23 | AA16674 |
| 28 | 315   | 23.0 | 289 | 23 | AA16674 |
| 29 | 315   | 23.0 | 296 | 23 | AA15424 |
| 30 | 315   | 23.0 | 303 | 22 | AA15444 |
| 31 | 315   | 23.0 | 303 | 22 | AA15037 |
| 32 | 313   | 22.9 | 285 | 21 | AA15331 |
| 33 | 309   | 22.6 | 289 | 22 | AA15037 |
| 34 | 308   | 22.5 | 289 | 23 | AA17230 |
| 35 | 306   | 22.4 | 314 | 23 | AA14187 |
| 36 | 306   | 22.4 | 331 | 22 | AA19557 |
| 37 | 304   | 22.2 | 285 | 21 | AA13023 |
| 38 | 304   | 22.2 | 285 | 21 | AA15432 |
| 39 | 304   | 22.2 | 285 | 22 | AA15037 |
| 40 | 297.5 | 21.8 | 225 | 23 | AA18058 |
| 41 | 297.5 | 21.8 | 244 | 18 | AA10910 |
| 42 | 296.5 | 21.7 | 260 | 21 | AA19152 |
| 43 | 296.5 | 21.7 | 287 | 21 | AA19166 |
| 44 | 294   | 21.5 | 247 | 18 | AA10910 |
| 45 | 294   | 21.5 | 247 | 22 | AA10528 |

#### ALIGNMENTS

|          |  |                            |
|----------|--|----------------------------|
| RESULT 1 | AA15548  | standard; Protein; 246 AA. |
| ID       | AA15548  |                            |
| AC       | AA15548  |                            |
| DT       | 28-FEB-2001  | (first entry)              |
| XX       |  |                            |
| DE       | Human immune system molecule from Incyte clone 1890540.                  |                            |
| XX       |  |                            |
| KM       | Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianemic;     |                            |
| KM       | antiartherosclerotic; antidiabetic; nephrotropic; cancer;                |                            |
| KM       | antigout; dermatological; antihypertensive; hepatotropic; antibacterial; |                            |
| KM       | immunosuppressive; cytotoxic; fungicide; protozoacide; antibacterial;    |                            |
| KM       | gene therapy; diagnostic; immunological disorder; viral infection;       |                            |
| KM       | bacterial infection; fungal infection; parasitic infection; immunogen.   |                            |
| OS       | Homo sapiens.  |                            |
| XX       |  |                            |
| PN       | WO200006080-A2.  |                            |
| XX       |  |                            |
| PD       | 12-OCT-2000.   |                            |
| XX       |  |                            |
| PF       | 04-APR-2000; 2000WO-US09072.   |                            |
| XX       |  |                            |
| PR       | 05-APR-1999; 99US-0127852.   |                            |
| PR       | 05-MAY-1999; 99US-0132647.   |                            |
| XX       |  |                            |
| PA       | (INCYTE) INCYTE PHARM INC.   |                            |
| XX       |  |                            |
| PI       | Yue H, Lai P, Tang YT, Baughn MR, Azimzai Y, Lu DAM;                     |                            |
| XX       |  |                            |
| DR       | WPI, 2000-665005/64.   |                            |



DR N-PSDB: AAA95787.  
 XX New human immune system molecules 1-15 and polynucleotides encoding  
 PT them useful for diagnosing, treating or preventing e.g. immunological  
 PT disorders, infections, cell proliferative disorders, microbial  
 PT infections  
 XX  
 XX  
 PS Claim 1: Page 85; 95pp; English.

XX This sequence represents a human immune system molecule (IMOL) encoded  
 CC by the cDNA isolated as clone 1890540 from the Incyte BLA07 library.  
 CC The human IMOLs (AAB15536-B15550) and their encoding polynucleotides  
 CC (AAA95775-95789), and compositions comprising them are useful for the  
 CC diagnosis, treatment or prevention of immunological disorders,  
 CC infections and cell proliferative disorders, including cancer. The IMOL  
 CC may be used to treat or prevent disorders associated with decreased  
 CC expression or activity of IMOL, such as immunological disorders  
 CC (e.g. inflammation, actinic keratosis, AIDS, Addison's disease),  
 CC hematopoietic cancer, infections caused by virus (e.g. adenovirus,  
 CC parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus,  
 CC Shigella), fungi (e.g. Aspergillus, Blastomycetes), parasites (e.g.  
 CC Plasmodium, Trypanosoma, intestinal protozoa), cell proliferative  
 CC disorders (e.g. actinic keratosis, arteriosclerosis, psoriasis), and  
 CC cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also  
 CC useful as immunogens for the development of antibodies that  
 CC specifically recognize these peptides. The polynucleotides may be used  
 CC to detect and quantify gene expression in biopsied tissues in which  
 CC expression of IMOL may be correlated with the disease, as targets in a  
 CC microarray, to detect differences in gene sequences among normal,  
 CC carrier and affected individuals, and for screening libraries of  
 CC compounds in drug screening techniques. Antibodies which specifically  
 CC bind to IMOL may be used for the diagnosis of disorders characterized  
 CC by expression of IMOL, or in assays to monitor patients being treated  
 CC with IMOL or agonists, antagonists, or inhibitors of IMOL.  
 CC  
 XX

SO Sequence 246 AA:

Query Match 100.0%; Score 1367; DB 21: Length 246;  
 Best Local Similarity 100.0%; Pred. No. 2e-124;  
 Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | MLMRRLTYWQLLALFLPCLCODEYMESPQTGGLRPDCKCHGQVSPFGYGPPEPPG      | 60  |
| DB | 1   | MLMRRLTYWQLLALFLPCLCODEYMESPQTGGLRPDCKCHGQVSPFGYGPPEPPG      | 60  |
| QY | 61  | PGICPGHNGNNGATGHEGAKGEGKDGDLPRGREGOHGKGEKGYGCIPELQIAF        | 120 |
| DB | 61  | PGICPGHNGNNGATGHEGAKGEGKDGDLPRGREGOHGKGEKGYGCIPELQIAF        | 120 |
| QY | 121 | MASLATHFSNQNSGIIFFSSVETNIGNFEDVMTGRFGAPVSGVYFFTFSSMKHEDVEEYV | 180 |
| DB | 121 | MASLATHFSNQNSGIIFFSSVETNIGNFEDVMTGRFGAPVSGVYFFTFSSMKHEDVEEYV | 180 |
| QY | 181 | YLMHNGNTVFSMTSTEMKKSQTSNNHAYLKLAKGDEWVLRMGALHGHORFSPAGF      | 240 |
| DB | 181 | YLMHNGNTVFSMTSTEMKKSQTSNNHAYLKLAKGDEWVLRMGALHGHORFSPAGF      | 240 |
| QY | 241 | LLEFETK 246  |     |
| DB | 241 | LLEFETK 246  |     |

RESULT 2  
 AAB29580  
 ID AAB29580 standard: Protein; 246 AA.

|    |   |
|----|---|
| XX | AAB29580;   |
| AC |   |
| XX |   |
| DT | 19-FEB-2001 (first entry)   |
| XX |   |
| DE | Human adipocyte complement related protein homologue zacrp3, SEQ ID NO.2. |
| XX |   |
| KW | Human zacrp3; adipocyte complement related protein homologue;             |

KW ACRP30; C1q domain; collagen-like domain; energy balance modulation;  
 KW cellular metabolism; metabolic disorder; obesity; anorexia;  
 KW antimicrobial agent; infection; platelet aggregation inhibition;  
 KW adhesion; activation; vascular injury; antibacterial; antiviral.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200063377-A1.  
 XX  
 XX 26-OCT-2000.  
 XX  
 XX 19-APR-2000; 2000WO-US10454.  
 XX  
 XX 20-APR-1999; 9905-0294943.  
 XX  
 XX (ZYMO) ZYMOGENETICS INC.  
 XX  
 XX Piddington CS, Bishop PD;  
 XX  
 XX WPI: 2000-665243/64.  
 DR N-PSDB: AAC64058.

PT Novel zacrp3 polypeptides used to treat or prevent bacterial or viral  
 PT infections, for wound healing, improving blood flow, and to analyze  
 PT energy efficiency in mammals.  
 XX  
 XX  
 PS Claim 2: Page 109-110; 123pp; English.

XX The invention relates to the human zacrp3 protein (AAB29580) and to  
 CC nucleic acids which encode it (AAC64058, AAC64053). Zacrp3 is a homologue  
 CC of adipocyte complement related protein (ACRP30) and contains  
 CC collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a  
 CC C-terminal C1q domain comprising 10 beta-strands. The zacrp3 gene is  
 CC located on chromosome 5p12. The invention also relates to zacrp3  
 CC fragments, fusion proteins containing zacrp3 polypeptides,  
 CC zacrp3-specific antibodies, expression constructs and host cells  
 CC comprising zacrp3 nucleic acids, and methods of recombinant production of  
 CC zacrp3. Human zacrp3, and its agonists and antagonists may be used in the  
 CC study and modulation of cellular metabolism and energy balance in  
 CC mammals, and may therefore be used to treat disorders such as obesity and  
 CC anorexia, and conditions associated with these disorders. Due to its C1q  
 CC like domain, zacrp3 and zacrp3-containing fusion proteins may be useful  
 CC as antimicrobial agents, promoting lysis or phagocytosis of infections  
 CC organisms such as bacteria or viruses. Zacrp3, its fragments, fusion  
 CC proteins, antibodies and activity modulators may also be used to inhibit  
 CC collagen-induced platelet aggregation, adhesion, or activation, and may  
 CC therefore have potential for promoting blood flow within the vasculature  
 CC of a mammal e.g., to treat injury to the vasculature or other collagenous  
 CC tissue. Human zacrp3 and its antibodies may additionally be used to study  
 CC dimerisation and oligomerisation. The present sequence represents human  
 CC zacrp3.  
 CC  
 XX

SO Sequence 246 AA:  
 Query Match 100.0%; Score 1367; DB 21: Length 246;  
 Best Local Similarity 100.0%; Pred. No. 2e-124;  
 Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | MLMRRLTYWQLLALFLPCLCODEYMESPQTGGLRPDCKCHGQVSPFGYGPPEPPG      | 60  |
| DB | 1   | MLMRRLTYWQLLALFLPCLCODEYMESPQTGGLRPDCKCHGQVSPFGYGPPEPPG      | 60  |
| QY | 61  | PGICPGHNGNNGATGHEGAKGEGKDGDLPRGREGOHGKGEKGYGCIPELQIAF        | 120 |
| DB | 61  | PGICPGHNGNNGATGHEGAKGEGKDGDLPRGREGOHGKGEKGYGCIPELQIAF        | 120 |
| QY | 121 | MASLATHFSNQNSGIIFFSSVETNIGNFEDVMTGRFGAPVSGVYFFTFSSMKHEDVEEYV | 180 |
| DB | 121 | MASLATHFSNQNSGIIFFSSVETNIGNFEDVMTGRFGAPVSGVYFFTFSSMKHEDVEEYV | 180 |
| QY | 181 | YLMHNGNTVFSMTSTEMKKSQTSNNHAYLKLAKGDEWVLRMGALHGHORFSPAGF      | 240 |
| DB | 181 | YLMHNGNTVFSMTSTEMKKSQTSNNHAYLKLAKGDEWVLRMGALHGHORFSPAGF      | 240 |

OY 241 LLEFETK 246  
Db 241 LLEFETK 246

RESULT 3  
AAB18909  
ID AAB18909 standard; Protein: 246 AA.

XX AAB18909;

XX 08-FEB-2001 (first entry)

DE A novel polypeptide designated PRO1484.

XX Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;  
KM PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;  
KM PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;  
KM PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;  
KM insulinemia; kidney disorder; Bergers disease; nephropathy;  
KM Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis;  
KM Crohns disease.

XX Homo sapiens.

XX Location/Qualifiers

FT Key

FT Peptide

FT /note= "signal peptide"

FT /note= "Clq domain protein"

FT /note= "Clq domain protein"

FT /note= "Clq domain protein"

FT /note= "Clq domain protein"

FT /note= "Clq domain protein"

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PR 27-APR-1999; 99US-0131272.  
PR 27-APR-1999; 99US-0131291.  
PR 04-MAY-1999; 99US-0132371.  
PR 04-MAY-1999; 99US-0132379.  
PR 04-MAY-1999; 99US-0132383.  
PR 25-MAY-1999; 99US-0135750.  
PR 08-JUN-1999; 99US-0138166.  
PR 20-JUL-1999; 99US-0144791.  
PR 03-AUG-1999; 99US-0146970.  
PR 09-DEC-1999; 99US-0170262.

XX (GETH ) GENENTECH INC.

XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;

PI Stewart TA, Watanabe CK, Wood WJ, Zhang Z;

XX WPI: 2000-628263/60.

DR N-PSDB: AAA96336.

XX Novel secreted and transmembrane polypeptides useful for diagnosing

PT tumour in a mammal, for identifying agonists and antagonists of the

PT polypeptide and for therapeutic use

XX Claim 12; Fig 2; 222pp; English.

XX The present sequence represents a secreted or transmembrane polypeptide.

XX The specification describes polypeptides designated PRO1484, PRO4334,

CC PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,

CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,

CC PRO6030, PRO4424, PRO4430 and PRO4499. PRO1889 polypeptide is

CC useful for diagnosing tumour in a mammal. The polypeptides, their

CC agonists and antagonists are useful treating a condition associated with

CC expression or activity of the polypeptide. Conditions treated include

CC obesity, diabetes or hyper- or hypo- insulinemia. The polypeptides are

CC capable of inducing proliferation of mammalian kidney mesangial cells

CC and are therefore useful for treating kidney disorders associated with

CC decreased mesangial cell function such as Bergers disease or other

CC nephropathies associated with Schonlein-Henoch purpura, celiac disease,

CC dermatitis herpetiformis or Crohns disease. The nucleic acids may be used

CC to generate transgenic animals for use in development and screening of

CC therapeutically useful reagents and also for chromosome identification

CC and tissue typing.

XX Sequence 246 AA:

XX

XX

XX

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XX

XX

XX

XX

XX

Query Match 100.0%; Score 1367; DB 21; Length 246;

Best Local Similarity 100.0%; Pred. No. 2e-124;

Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLRROLIYWQALLAFPLPCLODEYMESPOTGGLPPDCSKCHGDPSPFGYGGPPPG 60

1 MLRROLIYWQALLAFPLPCLODEYMESPOTGGLPPDCSKCHGDPSPFGYGGPPPG 60

61 PGIPGNHNGNNGATGHEGAKGKGDGLPRGGRGHPGKGEKGYGIPPELQIAP 120

61 PGIPGNHNGNNGATGHEGAKGKGDGLPRGGRGHPGKGEKGYGIPPELQIAP 120

121 MASLATHFSNONGIIFSSVETNIGNFDVMTGRFGAPVSGVYFFTFSMKHEDVEEYV 180

121 MASLATHFSNONGIIFSSVETNIGNFDVMTGRFGAPVSGVYFFTFSMKHEDVEEYV 180

121 MASLATHFSNONGIIFSSVETNIGNFDVMTGRFGAPVSGVYFFTFSMKHEDVEEYV 180

121 MASLATHFSNONGIIFSSVETNIGNFDVMTGRFGAPVSGVYFFTFSMKHEDVEEYV 180

181 YLMHNGNTVFSWYSYEMKKGSDPSSNHAVALKLAKGDEVLMRMGALHGHOFSTFAGF 240

181 YLMHNGNTVFSWYSYEMKKGSDPSSNHAVALKLAKGDEVLMRMGALHGHOFSTFAGF 240

241 LLEFETK 246

241 LLEFETK 246

241 LLEFETK 246

241 LLEFETK 246

241 LLEFETK 246

241 LLEFETK 246

241 LLEFETK 246

241 LLEFETK 246

241 LLEFETK 246

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241 LLEFETK 246

241 LLEFETK 246

241 LLEFETK 246

241 LLEFETK 246

RESULT 4  
AAB88447  
ID AAB88447 standard; Protein: 246 AA.

XX AAB88447;  
 AC  
 DT 23-MAY-2001 (first entry)  
 XX  
 DE Human membrane or secretory protein clone PSEC0232.  
 XX  
 KW Human: secretory protein; membrane protein; vaccine; gene therapy;  
 XX rheumatoid arthritis; diabetes.  
 OS Homo sapiens.  
 XX  
 PN EPI067182-A2.  
 XX  
 PD 10-JAN-2001.  
 XX  
 PF 07-JUL-2000; 2000EP-0114090.  
 XX  
 PR 08-JUL-1999; 99JP-0194179.  
 PR 11-JAN-2000; 2000JP-0118775.  
 PR 02-MAY-2000; 2000JP-0183766.  
 XX  
 PA (HELI-) HELIX RES INST.  
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
 DR WPI: 2001-093989/11.  
 DR N-PSDB: AAF93874.  
 XX  
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in  
 PT gene therapy or as candidate target molecules in drug development -  
 XX  
 PS Claim 1; SEQ ID 262; 609pp + CD ROM; English.  
 XX  
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916  
 CC which encode human secretory or membrane proteins represented by  
 CC AAB88317 - AAB88419. Included in the invention are primers  
 CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the  
 CC cDNA sequences of the invention. The invention also includes methods for  
 CC the production of antibodies directed against the proteins, and cDNA  
 CC sequences, which can be used in vaccines. The polynucleotide sequences  
 CC can be used in gene therapy. The polynucleotide sequences and the  
 CC proteins they encode may be used in the prevention, treatment and  
 CC diagnosis of diseases associated with inappropriate secretory  
 CC protein/membrane protein expression. The nucleic acids and complementary  
 CC sequences may also be used as DNA probes in diagnostic assays  
 CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the  
 CC presence of similar nucleic acid sequences in samples. They may also be  
 CC used to study the expression and function of secretory proteins/membrane  
 CC polypeptides and their role in metabolism. The polypeptides may be used  
 CC as antigens in the production of antibodies against them and in assays to  
 CC identify modulators (agonists and antagonists) of expression and  
 CC activity. The antibodies and antagonists may also be used as therapeutic  
 CC agents to down regulate expression and activity. The antibodies may also  
 CC be used as diagnostic agents for detecting the presence of the  
 CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay  
 CC (ELISA)). Examples of diseases which may be treated include rheumatoid  
 CC arthritis and diabetes.  
 CC  
 SQ Sequence 246 AA;  
 XX  
 Query Match 100.0%; Score 1367; DB 22; Length 246;  
 Best Local Similarity 100.0%; Pred. No. 2e-124;  
 Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MLMRLIYQQLALFLFPCQLQDEYMSPTQGLPPDCSKCHDYSFRGYQGPFG 60  
 DB 1 MLMRLIYQQLALFLFPCQLQDEYMSPTQGLPPDCSKCHDYSFRGYQGPFG 60  
 OY 61 PPGIGNNGNNGNNGATGHEGAKGKGKGDJGPRGGRGQHHPKGEKGYGPIPELQIAF 120  
 DB 61 PPGIGNNGNNGNNGATGHEGAKGKGKGDJGPRGGRGQHHPKGEKGYGPIPELQIAF 120

OY 121 MASLATHFSNONGIIFSSVETNIGNPFDMVMTGRGAPVSGVYFFTFSSMKHEDVEEYV 180  
 DB 121 MASLATHFSNONGIIFSSVETNIGNPFDMVMTGRGAPVSGVYFFTFSSMKHEDVEEYV 180  
 OY 181 YLMHNGNTVFSMYSEMKKSDTSSNHAVALKAKDEYWLRMGNCALHGDHGFSTFAGF 240  
 DB 181 YLMHNGNTVFSMYSEMKKSDTSSNHAVALKAKDEYWLRMGNCALHGDHGFSTFAGF 240  
 OY 241 LLEFRK 246  
 DB 241 LLEFRK 246

## RESULT 5

AA084371  
 ID AA084371 standard; Protein: 246 AA.

AA084371;  
 AC  
 XX  
 DT 08-MAY-2002 (first entry)

DE Novel human secreted or membrane-associated protein #10.

KW Human: secreted protein; membrane-associated protein; hypertension;  
 KW inflammatory disorder; neurological disorder; haematopoietic disorder;  
 KW skeletal developmental disorder; growth abnormality; autoimmune disorder;  
 KW neurodegenerative disorder; nervous system disorder; bacterial infection;  
 KW peripheral myelinopathy; viral infection; cancer; obesity; diabetes;  
 KW hypotension; sexual development disorder; blood disorder.

XX Homo sapiens.  
 OS  
 XX  
 PN WO200204600-A2.  
 XX  
 PD 17-JAN-2002.  
 XX  
 PF 12-JUL-2001; 2001WO-US21985.  
 PR 12-JUL-2000; 2000US-218033P.  
 PR 21-AUG-2000; 2000US-226517P.

XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA (GLAXO ) GLAXO GROUP LTD.  
 XX  
 PI Agarwal P, Cogswell JP, Lai Y, Martensen SA, Rizvi SK, Strum JC;  
 PI Smith R, Xiang Z, Xie Q;  
 DR WPI: 2002-188468/24.  
 DR N-PSDB: ABK35591.

XX Novel secreted and membrane-associated polypeptides and polynucleotides  
 PT encoding the polypeptides, for preventing, treating and ameliorating  
 PT cancers, mental or sexual developmental disorders, and malignant tumours  
 PT

Claim 1; Page 131-132; 151pp; English.

XX The present invention relates to the isolation of novel human secreted  
 CC or membrane-associated proteins and the genes encoding them. The  
 CC sequences of the invention are useful for treating, preventing and  
 CC ameliorating various diseases such as inflammatory disorders (e.g.  
 CC asthma), neurological disorders (e.g. dementia), haematopoietic  
 CC disorders, skeletal developmental disorders, growth abnormalities,  
 CC neurodegenerative disorders (e.g. Huntington's disease), nervous system  
 CC disorders, autoimmune disorders (e.g. rheumatoid arthritis),  
 CC peripheral myelinopathies, viral and bacterial infections,  
 CC alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and  
 CC hypotension, obesity, bulimia, anorexia, manic depression, delirium,  
 CC mental retardation, Tourette's syndrome, schizophrenia, growth, mental  
 CC or sexual development disorders, and dysfunctions of the blood cascade  
 CC system including those leading to stroke. AA084362-AA084389 represent  
 CC the novel human secreted or membrane-associated proteins of the

CC invention.  
XX  
SQ Sequence 246 AA:  
Query Match 100.0%; Score 1367; DB 23; Length 246;  
Best Local Similarity 100.0%; Pred. No. 2e-124; Mismatches 0; Indels 0; Gaps 0;  
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLMROLIYWOLLALEFLPFCLOCODEYMEPOTGGLPPDCSKCHDYSPFRGYPGPPG 60  
Db 1 MLMROLIYWOLLALEFLPFCLOCODEYMEPOTGGLPPDCSKCHDYSPFRGYPGPPG 60  
QY 61 PPGIGNHNNGNNGATGHEGAKGKGDGLGPRGERGQHGPKEKYPGIPPELQIAF 120  
Db 61 PPGIGNHNNGNNGATGHEGAKGKGDGLGPRGERGQHGPKEKYPGIPPELQIAF 120  
QY 121 MASLATHFSNONGIIFSSVEFTNIGNFPDVMTRGAPVSGYFFTFSMKHEDVEEYV 180  
Db 121 MASLATHFSNONGIIFSSVEFTNIGNFPDVMTRGAPVSGYFFTFSMKHEDVEEYV 180  
QY 181 YLMHNGNTVFSYSEMKGKSDTSSNHAVALKLAKGDEVLMRMGNCALHGDHQRSTFAGF 240  
Db 181 YLMHNGNTVFSYSEMKGKSDTSSNHAVALKLAKGDEVLMRMGNCALHGDHQRSTFAGF 240  
QY 241 LLEFETK 246  
Db 241 LLEFETK 246  
RESULT 6  
ID AA084370 standard; Protein: 319 AA.  
AC AA084370;  
XX 08-MAY-2002 (first entry)  
DE Novel human secreted or membrane-associated protein #9.  
XX  
KW Human; secreted protein; membrane-associated protein; hypertension;  
inflammatory disorder; neurological disorder; haematopoietic disorder;  
skeletal developmental disorder; growth abnormality; autoimmune disorder;  
neurodegenerative disorder; nervous system disorder; bacterial infection;  
peripheral myelinopathy; viral infection; cancer; obesity; diabetes;  
hypotension; sexual development disorder; blood disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200204600-A2.  
PD 17-JAN-2002.  
XX  
PE 12-JUL-2001; 2001WO-US21985.  
XX  
PR 12-JUL-2000; 2000US-218033P.  
PR 21-AUG-2000; 2000US-226517P.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (GLAXO ) GLAXO GROUP LTD.  
PI Agarwal P, Cogswell JP, Lai Y, Martensen SA, Rizvi SK, Strum JC;  
PI Smith RF, Xiang Z, Xie Q;  
XX WPI: 2002-188468/24.  
DR N-PSDB: ABR35390.  
XX  
XX Novel secreted and membrane-associated polypeptides and polynucleotides  
encoding the polypeptides, for preventing, treating and ameliorating  
PT cancers, mental or sexual developmental disorders, and malignant tumours  
PT  
PS Claim 1; Page 130-131; 151pp; English.

XX  
CC The present invention relates to the isolation of novel human secreted  
CC or membrane-associated proteins and the genes encoding them. The  
CC sequences of the invention are useful for treating, preventing and  
CC ameliorating various diseases such as inflammatory disorders (e.g.  
CC asthma), neurological disorders (e.g. dementia), haematopoietic  
CC disorders, skeletal developmental disorders, growth abnormalities,  
CC neurodegenerative disorders (e.g. Huntington's disease), nervous system  
CC disorders, autoimmune disorders (e.g. rheumatoid arthritis),  
CC peripheral myelinopathies, viral and bacterial infections,  
CC alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and  
CC hypotension, obesity, bulimia, anorexia, manic depression, delirium,  
CC mental retardation, Tourette's syndrome, schizophrenia, growth, mental  
CC or sexual development disorders, and dysfunctions of the blood cascade  
CC system including those leading to stroke. AA084362-AA084389 represent  
CC the novel human secreted or membrane-associated proteins of the  
CC invention.  
XX  
SQ Sequence 319 AA;  
Query Match 96.6%; Score 1320.5; DB 23; Length 319;  
Best Local Similarity 77.1%; Pred. No. 9.3e-120;  
Matches 246; Conservative 0; Mismatches 0; Indels 73; Gaps 1;  
QY 1 MLMROLIYWOLLALEFLPFCLOCODEYME-----SPOTGGLPPDCSKCHDY 28  
Db 1 MLMROLIYWOLLALEFLPFCLOCODEYME-SGRTNKVARIYQSHOQTRSGSRRKVRER 60  
QY 29 -----  
Db 61 SHPKTGYDNNSTDLKLRLDELPHPREVDDLAQITTTWGSPPOTGGLPPDCSKCHDY 120  
QY 48 SFRGYGPPGPPGPPGIPGNHNGNNGATGHEGAKGKGDGLGPRGERGQHGPKEK 107  
Db 121 SFRGYGPPGPPGPPGIPGNHNGNNGATGHEGAKGKGDGLGPRGERGQHGPKEK 180  
QY 108 GYPGIPPELQIAFNASLATHFSNONGIIFSSVEFTNIGNFPDVMTRGAPVSGYFFTF 167  
Db 181 GYPGIPPELQIAFNASLATHFSNONGIIFSSVEFTNIGNFPDVMTRGAPVSGYFFTF 240  
QY 168 SMKHEDVEEYVYLMHNGNTVFSYSEMKGKSDTSSNHAVALKLAKGDEVLMRMGNCAL 227  
Db 241 SMKHEDVEEYVYLMHNGNTVFSYSEMKGKSDTSSNHAVALKLAKGDEVLMRMGNCAL 300  
QY 228 HGDHQRSTFAGFLLEFETK 246  
Db 301 HGDHQRSTFAGFLLEFETK 319  
RESULT 7  
ID AAB29582 standard; Protein: 246 AA.  
AC AAB29582;  
XX 19-FEB-2001 (first entry)  
XX  
DE Mouse zacr2 protein, SEQ ID NO:12.  
XX  
XX Mouse zacr2; adipocyte complement related protein homologue;  
KW ACRP30; C1q domain; collagen-like domain; energy balance modulation;  
KW cellular metabolism; metabolic disorder; obesity; anorexia;  
KW antimicrobial agent; infection; platelet aggregation inhibition;  
KW adhesion; activation; vascular injury; antibacterial; antiviral;  
KW human zacr2 homologue.  
XX  
XX Mus musculus.  
OS  
XX  
PN WO2000063377-A1.  
XX 26-OCT-2000.  
XX  
PF 19-APR-2000; 2000WO-US10454.

XX 20-APR-1999; 99US-0294943.  
XX (ZYMO ) ZYMOGENETICS INC.  
XX Piddington CS, Bishop PD;  
XX MPI: 2000-665243/64.  
XX N-PSDB: AAC64064.  
XX  
XX Novel zacr3 polypeptides used to treat or prevent bacterial or viral  
XX infections, for wound healing, improving blood flow, and to analyze  
XX energy efficiency in mammals -  
XX  
XX Disclosure; Page 117-118; 123pp; English.  
XX  
XX The invention relates to the human zacr3 protein (AAB29580) and to  
XX nucleic acids which encode it (AAC64058, AAC64063). Zacr3 is a homologue  
XX of adipocyte complement related protein (ACRP30) and contains a  
XX collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a  
XX C-terminal C1q domain comprising 10 beta-strands. The zacr3 gene is  
XX located on chromosome 5p12. The invention also relates to zacr3  
XX fragments, fusion proteins containing zacr3 polypeptides,  
XX zacr3-specific antibodies, expression constructs and host cells  
XX comprising zacr3 nucleic acids, and methods of recombinant production of  
XX zacr3. Human zacr3, and its agonists and antagonists may be used in the  
XX study and modulation of cellular metabolism and energy balance in  
XX mammals, and may therefore be used to treat disorders such as obesity and  
XX anorexia, and conditions associated with these disorders. Due to its C1q  
XX like domain, zacr3 and zacr3-containing fusion proteins may be useful  
XX as antimicrobial agents, promoting lysis or phagocytosis of infectious  
XX organisms such as bacteria or viruses. Zacr3, its fragments, fusion  
XX proteins, antibodies and activity modulators may also be used to inhibit  
XX collagen-induced platelet aggregation, adhesion, or activation, and may  
XX therefore have potential for promoting blood flow within the vasculature  
XX of a mammal e.g., to treat injury to the vasculature or other collagenous  
XX tissue. Human zacr3 and its antibodies may additionally be used to study  
XX dimerisation and oligomerisation. The present sequence represents mouse  
XX zacr3, a homologue of human zacr3.  
XX  
XX Sequence 246 AA:  
SO  
Query Match 95.94; Score 1311; DB 21; Length 246;  
Best Local Similarity 95.94; Pred. No. 5.5e-119;  
Matches 236; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
QY 1 MLMKQLYMWLLAFLEPFLCQDEYHESPTGGLPPDCSCCHGDSFRGYPGPPG 60  
DB 1 MGRQRIMWHMLPLFLPFLCQDEYHESPTGGLPPDCSCCHGDSFRGYPGPPG 60  
QY 61 PPGIPGHHNGNNGANGHGEKGEKDKDGLGRGEGHGRGEGKGPRIPELQIAF 120  
DB 61 PPGIPGHHNGNNGANGHGEKGEKDKDGLGRGEGHGRGEGKGPRIPELQIAF 120  
QY 121 MASLATHFSNONGSIIFSSVETNIGNEFDVMTGRFGAPVSGVYFTFSMKHEDVEEYV 180  
DB 121 MASLATHFSNONGSIIFSSVETNIGNEFDVMTGRFGAPVSGVYFTFSMKHEDVEEYV 180  
QY 181 YLMHNGTVFSMSYSEKMSKSDTSSNHAVALKLAKGDEVYLMRGKALGHQRETFAGF 240  
DB 181 YLMHNGTVFSMSYSEKMSKSDTSSNHAVALKLAKGDEVYLMRGKALGHQRETFAGF 240  
QY 241 LLEFTK 246  
DB 241 LLEFTK 246  
RESULT 8  
ID AAM99925 standard; Protein: 225 AA.  
XX AAM99925;  
XX

DT 07-JAN-2002 (first entry)  
XX  
XX Human polypeptide SEQ ID NO 41.  
DE  
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
XX anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antitumor;  
XX vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
XX cardiatic; gene therapy; cancer; immune disorder; cardiovascular disorder;  
XX neurological disease; infection; human; secreted protein.  
OS  
XX Homo sapiens.  
XX  
XX MO200155173-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001MO-US01356.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
XX 04-FEB-2000; 2000US-0180628.  
XX 24-FEB-2000; 2000US-0184664.  
XX 02-MAR-2000; 2000US-0186350.  
XX 16-MAR-2000; 2000US-0189874.  
XX 17-MAR-2000; 2000US-0190076.  
XX 18-APR-2000; 2000US-0198123.  
XX 19-MAY-2000; 2000US-0205515.  
XX 07-JUN-2000; 2000US-0209467.  
XX 28-JUN-2000; 2000US-0214886.  
XX 30-JUN-2000; 2000US-0215135.  
XX 07-JUL-2000; 2000US-0216647.  
XX 07-JUL-2000; 2000US-0216880.  
XX 11-JUL-2000; 2000US-0217487.  
XX 11-JUL-2000; 2000US-0217486.  
XX 14-JUL-2000; 2000US-0218280.  
XX 26-JUL-2000; 2000US-0220963.  
XX 26-JUL-2000; 2000US-0220964.  
XX 14-AUG-2000; 2000US-0224518.  
XX 14-AUG-2000; 2000US-0224519.  
XX 14-AUG-2000; 2000US-0225213.  
XX 14-AUG-2000; 2000US-0225214.  
XX 14-AUG-2000; 2000US-0225266.  
XX 14-AUG-2000; 2000US-0225267.  
XX 14-AUG-2000; 2000US-0225268.  
XX 14-AUG-2000; 2000US-0225270.  
XX 14-AUG-2000; 2000US-0225447.  
XX 14-AUG-2000; 2000US-0225757.  
XX 14-AUG-2000; 2000US-0225758.  
XX 14-AUG-2000; 2000US-0225759.  
XX 18-AUG-2000; 2000US-0226279.  
XX 22-AUG-2000; 2000US-0226681.  
XX 22-AUG-2000; 2000US-0226868.  
XX 22-AUG-2000; 2000US-0227182.  
XX 23-AUG-2000; 2000US-0227009.  
XX 30-AUG-2000; 2000US-0228924.  
XX 01-SEP-2000; 2000US-0229287.  
XX 01-SEP-2000; 2000US-0229343.  
XX 01-SEP-2000; 2000US-0229344.  
XX 01-SEP-2000; 2000US-0229345.  
XX 05-SEP-2000; 2000US-0229509.  
XX 06-SEP-2000; 2000US-0230437.  
XX 06-SEP-2000; 2000US-0230438.  
XX 06-SEP-2000; 2000US-0231242.  
XX 08-SEP-2000; 2000US-0231243.  
XX 08-SEP-2000; 2000US-0231244.  
XX 08-SEP-2000; 2000US-0231413.  
XX 08-SEP-2000; 2000US-0231414.  
XX 08-SEP-2000; 2000US-0232080.  
XX 08-SEP-2000; 2000US-0232081.  
XX 12-SEP-2000; 2000US-0231968.  
XX 14-SEP-2000; 2000US-0232397.  
XX 14-SEP-2000; 2000US-0232398.  
XX 14-SEP-2000; 2000US-0232399.

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PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0234984.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.

PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2000US-0259678.

PR (HUMA-) HUMAN GENOME SCI INC.
PR XX
PR PI Rosen CA, Barash SC, Ruben SM;
PR DR WPI; 2001-451924/48.
PR XX N-PSDB; AA19523.
PR PT New nucleic acids and polypeptides, useful for treating, preventing or
PR PT ameliorating human disorders and diseases -
PR XX
PR XX Claim 11; SEQ ID NO 41; 465pp + Sequence Listing; English.
PR CC The invention relates to novel human polynucleotides (AA19513-AA19518)
PR CC and the encoded proteins (AA19515-AA19514) which are useful for
PR CC preventing, treating or ameliorating medical conditions e.g. by protein
PR CC or gene therapy. The genes are isolated from a range of human tissues
PR CC disclosed in the specification. The nucleic acids, proteins, antibodies
PR CC and (ant)agonists are useful in the diagnosis, treatment and prevention
PR CC of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
PR CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
PR CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,
PR CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
PR CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
PR CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as
PR CC myocardial ischaemias; (d) wound healing; (e) neurological diseases
PR CC e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as
PR CC viral, bacterial, fungal and parasitic infections.
PR CC Note: The sequence data for this patent did not form part of the
PR CC printed specification, but was obtained in electronic format directly
PR CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
PR XX
PR XX Sequence 225 AA:
PR SQ
PR Query Match 88.4%; Score 1208; DB 22; Length 225;
PR Best Local Similarity 99.5%; Pred. No. 4.9e-109;
PR Matches 218; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 28 ESPQTGGLPPDCSKCHDYSFRGYGPPGPPGPGIGTGNHNNNGNATGHEGAKGKG 87
DB 7 OSPTGGLPPDCSKCHDYSFRGYGPPGPPGPGIPGNIHNNNGNATGHEGAKGKG 66
QY 88 DKGDGPPRGGRGQHPKCEKGYPGIPELOIAFMASLATHFENONGSGLIFSSVETNIGNF 147
DB 67 DKGDGPPRGGRGQHPKCEKGYPGIPELOIAFMASLATHFENONGSGLIFSSVETNIGNF 126
QY 148 FDVMTGRFGAPYGVYFFTFSSMKHEDVEEYVYLMHNGNTVFSMYSEMKGSDTSSNH 207
DB 127 FDVMTGRFGAPYGVYFFTFSSMKHEDVEEYVYLMHNGNTVFSMYSEMKGSDTSSNH 186
QY 208 AVLKLAGDEWVLRMGNGALHGDHOFSTFAGFLLETRK 246
DB 187 AVLKLAGDEWVLRMGNGALHGDHOFSTFAGFLLETRK 225

RESULT 9
AA1860
ID AA1860 standard; Protein; 202 AA.
XX
XX AA1860;
AC
AC AA1860;
DT 22-OCT-2001 (first entry)
XX Human polypeptide SEQ ID NO 6791.
DE
XX
```





SO Sequence 223 AA; 58.0%; Score 792.5; DB 22; Length 223;  
 Query Match Best Local Similarity 66.8%; Pred. No. 1e-66;  
 Matches 147; Conservative 0; Mismatches 0; Indels 73; Gaps 1;

QY 1 MIMROLIYWQLLALFFLPCLCODEYME----- 28  
 DB 1 MIMROLIYWQLLALFFLPCLCODEYMEVSGRTNKVARIYOSHOOGRSGSRREKVRER 60  
 OY 29 -----SPOTGGLPPDCSKCHG DY 47  
 DB 61 SHPKGTGYNNTSTDLKSRPELPHPEYVDLAQTTFWGSPPQTGGLPDDCSKCHG DY 120

QY 48 SERGYGPPGPPGPPGIPGNHGNNGNATGHEGAKGEGKDGKDLGPRGEGQHGPKEG 107  
 DB 121 SPRGYGPPGPPGPPGIPGNHGNNGNATGHEGAKGEGKDGKDLGPRGEGQHGPKEG 180

QY 108 GYPGIPPELQIAFMASLATHSNONGIIFSSVETNIGNF 147  
 DB 181 GYPGIPPELQIAFMASLATHSNONGIIFSSVETNIGNF 220

RESULT 11  
 AAY1485  
 ID AAY1485 standard; Protein; 128 AA.  
 AC AAY1485;  
 XX 21-JUN-1999 (first entry)  
 DE Human 5' EST secreted protein SEQ ID NO 307.  
 XX Human; secreted protein; EST; expressed sequence tag; diagnosis;  
 KW forensic; gene therapy; chromosome mapping; signal peptide;  
 KW upstream regulatory sequence; cytokine activity; cell proliferation;  
 KW differentiation; haematopoiesis regulation; tissue growth regulation;  
 KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;  
 KW thrombolytic; anti-inflammatory; tumour inhibition.  
 XX Homo sapiens.  
 OS  
 XX MO9906551-A2.  
 PN 11-FEB-1999.  
 PD 31-JUL-1998; 98MO-IB01235.  
 PF 01-AUG-1997; 97US-0905133.  
 PR (GEST ) GENSET.  
 PA  
 PI Duclert A, Dumas Milne Edwards J, Lacroix B;  
 XX WPI; 1999-153781/13.  
 DR N-PSDB; AAX39551.  
 XX New nucleic acids encoding human secreted - proteins obtained from  
 PT cDNA libraries prepared from substantia nigra, cerebellum, surrenals  
 PT and fetal brain tissue  
 XX  
 PS Claim 34; Page 402-403; 434pp; English.  
 CC AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for  
 CC human secreted proteins, and encode the proteins given in AAY11374 to  
 CC AAY11531, respectively. The proteins given represent the signal peptide  
 CC and an N-terminal fragment of a secreted protein. The nucleic acid  
 CC sequences can be used for producing secreted human gene products. They  
 CC can also be used to develop products for diagnosis and therapy. The  
 CC proteins obtained may have cytokine activity, cell  
 CC proliferation/differentiation activity, haematopoiesis regulating  
 CC activity, tissue growth regulating activity, reproductive hormone  
 CC regulating activity, chemotactic/ chemokinetic activity, haemostatic and

CC thrombolytic activity, receptor/ ligand activity, anti-inflammatory  
 CC activity, tumour inhibition activity or other activities. The products  
 CC can be used in forensic, gene therapy and chromosome mapping procedures.  
 CC The sequences can also be used for obtaining corresponding promoter  
 CC sequences. The nucleic acids encoding the signal peptide can be used for  
 CC directing extracellular secretion of a polypeptide or the insertion of a  
 CC polypeptide into a membrane, or importing a polypeptide into a cell.  
 CC  
 SO Sequence 128 AA; 52.7%; Score 721; DB 20; Length 128;  
 Query Match Best Local Similarity 100.0%; Pred. No. 4.2e-62;  
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMROLIYWQLLALFFLPCLCODEYMESPTGGLPPDCSKCHG DYSPRGYGP GPPG 60  
 DB 1 MIMROLIYWQLLALFFLPCLCODEYMESPTGGLPPDCSKCHG DYSPRGYGP GPPG 60

QY 61 PPGIPGNHGNNGNATGHEGAKGEGKDGKDLGPRGEGQHGPKEGYPGIPPELQIAF 120  
 DB 61 PPGIPGNHGNNGNATGHEGAKGEGKDGKDLGPRGEGQHGPKEGYPGIPPELQIAF 120

QY 121 MASL 124  
 DB 121 MASL 124

RESULT 12  
 AAM40074  
 ID AAM40074 standard; Protein; 126 AA.  
 AC AAM40074;  
 XX 22-OCT-2001 (first entry)  
 DE Human polypeptide SEQ ID NO 3219.  
 XX Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX Homo sapiens.  
 OS  
 XX MO200153312-A1.  
 PN 26-JUL-2001.  
 PD 26-DEC-2000; 2000MO-US34263.  
 PF 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0596042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 XX  
 PA (HXSE-) HXSEQ INC.  
 XX  
 XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao Q, Zhou P, Goodrich R, Dimañac RT;  
 XX WPI; 2001-442253/47.  
 DR N-PSDB; AAI59230.  
 XX Novel nucleic acids and polypeptides useful for treating disorders  
 PT such as central nervous system injuries -



PT including wounds and cancer -

XX Claim 4; Page 168; 235pp; English.

CC The invention relates to novel nucleic acid sequences derived from rat  
CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,  
CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying  
CC cells. Polypeptides of the invention may be used to treat inflammation,  
CC cancer and neurological diseases. The proteins may be used to stimulate  
CC the growth and motility of keratinocytes, to inhibit the growth of  
CC cancer cells, to modulate angiogenesis and tumour vascularisation, to  
CC modulate skin inflammation, to modulate epithelial cell growth and to  
CC inhibit binding of HIV-1 to leukocytes. The invention may also be used  
CC to treat growth and developmental defects, skin wounds and hair follicle  
CC disorders. Sequences AAY75942-Y76123 represent polypeptides encoded  
CC by cDNA sequences derived from several mouse, rat or human skin cell  
CC types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and  
CC AAY76119 are proteins with an N-terminal signal sequence, indicating  
CC that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071,  
CC AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more  
CC putative transmembrane domains.

SO Sequence 105 AA:

Query Match 42.6%; Score 582; DB 21; Length 105;  
Best Local Similarity 93.3%; Pred. No. 1e-48;  
Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 MMRRLIYVQLALFPLPCLCODEYMESPOTGGLPPDCSKCHGYSFRGYGPPGPG 60

DB 1 MMRRLVMMHLALFLPCLCODEYMESPQAGLPPDCSKCHGDBGYGRGYGPPGPG 60

OY 61 PGIPGNHGNNGNGATGHEGAKGEKGDGLPRGERGQHGPKG 105

DB 61 PGIPGNHGNNGNGATGHEGAKGEKGDGLPRGERGQHGPKG 105

RESULT 15

AAB55908  
ID AAB55908 standard; Protein; 105 AA.

XX AAB55908;

DT 08-MAR-2001 (first entry)

DE Skin cell protein, SBO ID NO: 147.

XX Rat; skin cell; cytosolic; anti-inflammatory; anti-HIV;

KW neurotrophic; neuroprotective; vulnery; immunomodulatory; vaccine;

KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;

XX inflammation; neurological disease.

OS Rattus sp.

XX WO200069884-A2.

XX 23-NOV-2000.

XX 15-MAY-2000; 2000WO-NZ00075.

XX 14-MAY-1999; 99US-0312283.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;

XX WPI: 2001-007495/01.

XX N-PSDB: AAC95566, AAC99776.

XX New isolated polynucleotide used in the identification of genetic  
PT disorders and encoding polypeptides used for treating inflammatory  
PT disease, cancer and neurological diseases -

PS Claim 4; Page 147; 352pp; English.

CC The present sequence is a polypeptide which is expressed in  
CC mammalian skin cells. The polypeptide is useful for stimulating  
CC keratinocyte growth and motility, inhibiting the growth of cancer cells,  
CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of  
CC tumours, modulating skin inflammation, stimulating the growth of  
CC epithelial cells, inhibiting the binding of human immunodeficiency virus  
CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and  
CC neurological diseases. The polynucleotide can be used as a marker, in  
CC the identification of genetic disorders, and for the design of  
CC oligonucleotides for examining expression patterns.

SO Sequence 105 AA:

Query Match 42.6%; Score 582; DB 22; Length 105;  
Best Local Similarity 93.3%; Pred. No. 1e-48;  
Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 MMRRLIYVQLALFPLPCLCODEYMESPOTGGLPPDCSKCHGYSFRGYGPPGPG 60

DB 1 MMRRLVMMHLALFLPCLCODEYMESPQAGLPPDCSKCHGDBGYGRGYGPPGPG 60

OY 61 PGIPGNHGNNGNGATGHEGAKGEKGDGLPRGERGQHGPKG 105

DB 61 PGIPGNHGNNGNGATGHEGAKGEKGDGLPRGERGQHGPKG 105

Search completed: January 15, 2003, 19:37:10

Job time : 81 secs



;; CURRENT FILING DATE: 1998-11-09  
;; NUMBER OF SEQ ID NOS: 348  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 280  
;; LENGTH: 105  
;; TYPE: PRT  
;; ORGANISM: Rat  
US-09-188-930-280

Query Match 42.6%; Score 582; DB 4; Length 105;  
Best Local Similarity 93.3%; Pred. No. 2,1e-51;  
Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MMRRLIYVWLLALFLPFCICLDEYMEPOTGGLPPDCSKCHGDYSPFGYGPFGPPG 60  
DB 1 MMRRLIYVWLLALFLPFCICLDEYMEPOTGGLPPDCSKCHGDYSPFGYGPFGPPG 60  
QY 61 PPGIGNHGNNNGNNGATGHEGAKGKGGKDGIDGPRGRCQHGPKG 105  
DB 61 PPGIGNHGNNNGNNGATGHEGAKGKGGKDGIDGPRGRCQHGPKG 105

RESULT 3  
US-09-188-930-294  
; Sequence 294, Application US/09188930A  
; Patent No. 6150502  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murlison, James Greg  
; TITLE OF INVENTION: Compositions Isolated From Skin Cells  
; TITLE OF INVENTION: and Methods For Their Use  
; FILE REFERENCE: 11000,1011c1  
; CURRENT APPLICATION NUMBER: US/09/188, 930A  
; CURRENT FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 348  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 294  
; LENGTH: 294  
; TYPE: PRT  
; ORGANISM: Rat  
US-09-188-930-294

Query Match 23.1%; Score 316; DB 4; Length 294;  
Best Local Similarity 28.9%; Pred. No. 5,7e-24;  
Matches 86; Conservative 41; Mismatches 89; Indels 82; Gaps 12;

QY 6 LIYVWLLALFLPFCICLDEYMEPOTGGLPPDCSKCHGDYSPFGYGPFGPPG 59  
DB 10 MISMWLLALC-ALP---CAADPMLGAFARDDQKGGPOLVCS-----LPQPGGPP 54  
QY 60 GPPGIPGHNHNGNNGATGHEGAKGKGGKDG-----L 92  
DB 55 GPPGAPGSSGAWGRRGFGKDGQDQDGDSDGEGPPGRTGNRGKQGPKGKAGATGA 114  
QY 93 GPRGR-----GQHPKGEKGYPGIP-----PELOIAFMASLATHFSNONS 133  
DB 115 GPRGPKGVSGTPGKHGIPGKKGKGPKEGPGCLPGPCSGSSRAKSAFSAVATKSPRRL 174  
QY 134 GIIFSSVETNIGNFEFVDTGREGAPVSGVFEFTSM---KHEVVEEYVYVLMHNGNTVF 190  
DB 175 PIKFDKILAMGEGHYMASSGKFGVCSVFOITYFTDITLANKH-----LAICLVHNGO--Y 227  
QY 191 SMSYEEMK-GKSDTSSNHAVALKLAKGDEWLMR---GNGALHGDHOFSTFAGFLLE 243  
DB 228 RIRFDANTGCHHDVASSGTLILAKEGDEWMLQIFYSQNGCLFYDPYMTDSLFTGLIY 285

RESULT 4  
US-08-463-911-2  
; Sequence 2, Application US/08463911

;; Patent No. 5869310  
;; GENERAL INFORMATION:  
;; APPLICANT: Scherer, Philipp E.  
;; APPLICANT: Lodish, Harvey F.  
;; TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED  
;; TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES  
;; NUMBER OF SEQUENCES: 7  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.  
;; STREET: Two Militia Drive  
;; CITY: Lexington  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02173  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/463,911  
;; FILING DATE:  
;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Granahan, Patricia  
;; REGISTRATION NUMBER: 32,227  
;; TELEPHONE: (617) 861-9540  
;; TELEFAX: (617) 861-6240  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 247 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-463-911-2

Query Match 21.5%; Score 294; DB 2; Length 247;  
Best Local Similarity 31.5%; Pred. No. 7,4e-22;  
Matches 81; Conservative 40; Mismatches 102; Indels 34; Gaps 9;

QY 6 LIYVWLLALFLPFCICLDEYMEPOTGGLPPDCSKCHGDYSPFGYGPFGPPG 63  
DB 2 LILQALLFLILP-SHAEDVTTTELAPALVPPPKGTCA-----GMA-----GLPG 48  
QY 64 IPGNHNGNNGNNGATGHEGAKGKGGKDGIDGPRGR---GQHPKGEKGYPGIPPE----- 115  
DB 49 HPGNHGTGPRGDRGDTPEKEKEKGDAGLGPKEGTGDVGMGAEGRPGFPGRKGERG 108  
QY 116 -----LQIAFMASLATHFSNONSGLTSSVETNIGNFEFVDTGREGAPVSGVFEFTSM 170  
DB 109 EAAVMYRSASFVSGLETRVTPNVPIRFYKIFYNOONHNDGSGTKFYCNIPGLIYPSHYIT 168  
QY 171 KHEVVEEYVYVLMHNGNTVFMSYEMKGSJSSNHAVALKLAKGDEWLMR-GNG---A 226  
DB 169 VY--WKDVVSLFKKRAVLFTYDQYQEKNVDAQSVLLHLLEVDQWMLQYVGGDHNG 226  
QY 227 LHGDHOFSTFAGFLLE 243  
DB 227 LYADNVNDSTFTGLIY 243

RESULT 5  
US-09-530-423-2  
; Sequence 2, Application US/09530423  
; Patent No. 6461821  
; GENERAL INFORMATION:  
; APPLICANT: Otsuka Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a  
; TITLE OF INVENTION: diagnostic method for arteriosclerosis and a kit  
; FILE REFERENCE: P98-51

CURRENT APPLICATION NUMBER: US/09/530.423  
CURRENT FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: JP H9-297569  
PRIOR FILING DATE: 1997-10-29  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 231  
TYPE: PRT  
ORGANISM: Abdominal fat tissue from myoma uteri  
US-09-530-423-2

Query Match  
Best Local Similarity 34.5%; Score 293.5; DB 4; Length 231;  
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

OY 53 OGP-----PGPPG-----PGIPGNHNGNNGATGHEGAKGKGD---LGPR---GE 97  
DB 10 OGPVLLPLPKGACTGMMAGIPGPHNGAPRGDRDTPGKGEKGDPLGPKGDIGE 69  
OY 98 RGQHPKGEKGYPGI-----PPE---LQIAFMASLATHPSNONGIIFSSVETNIGNF 147  
DB 70 TGVPAEGPRGPGIQRKKEGEGAYVRSFVSGLTYTTPMPLRFTKITYNOQNH 129  
OY 148 EDVMTGRGAPYGVYFFFTSMKHEDEEYVYVLMHNGNTVFSMYSEMKKSDPTSSNH 207  
DB 130 YDGSIGKRFHCNIPGLYFAHYHTVY--MKDVVSLFKKDKAMLFYYDOYQENNVQASGS 187  
OY 208 AVLKAKGDEWLMR-GNG---ALHGDHORESTFAGFLIF 243  
DB 188 VLLHLEVGDDQVWLQYVYGEGERNGLYADNDNDSTFTGFLLY 227

RESULT 6  
US-08-463-911-7  
Sequence 7, Application US/08463911  
Patent No. 5869330  
GENERAL INFORMATION:  
APPLICANT: Scherer, Philipp E.  
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED  
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk.  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463.911  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: WHI95-05  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-9540  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-463-911-7

Query Match  
Best Local Similarity 21.5%; Score 293.5; DB 2; Length 244;  
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

OY 53 OGP-----PGPPG-----PGIPGNHNGNNGATGHEGAKGKGD---LGPR---GE 97  
DB 23 OGPVLLPLPKGACTGMMAGIPGPHNGAPRGDRDTPGKGEKGDPLGPKGDIGE 82  
OY 98 RGQHPKGEKGYPGI-----PPE---LQIAFMASLATHPSNONGIIFSSVETNIGNF 147  
DB 83 TGVPAEGPRGPGIQRKKEGEGAYVRSFVSGLTYTTPMPLRFTKITYNOQNH 142  
OY 148 EDVMTGRGAPYGVYFFFTSMKHEDEEYVYVLMHNGNTVFSMYSEMKKSDPTSSNH 207  
DB 143 YDGSIGKRFHCNIPGLYFAHYHTVY--MKDVVSLFKKDKAMLFYYDOYQENNVQASGS 200  
OY 208 AVLKAKGDEWLMR-GNG---ALHGDHORESTFAGFLIF 243  
DB 201 VLLHLEVGDDQVWLQYVYGEGERNGLYADNDNDSTFTGFLLY 240

RESULT 7  
US-09-140-804-3  
Sequence 3, Application US/09140804  
Patent No. 6197930  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
FILE REFERENCE: 97-49  
CURRENT APPLICATION NUMBER: US/09/140.804  
CURRENT FILING DATE: 1998-08-26  
EARLIER APPLICATION NUMBER: 60/056,983  
EARLIER FILING DATE: 1997-08-26  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 244  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-140-804-3

Query Match  
Best Local Similarity 21.5%; Score 293.5; DB 4; Length 244;  
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

OY 53 OGP-----PGPPG-----PGIPGNHNGNNGATGHEGAKGKGD---LGPR---GE 97  
DB 23 OGPVLLPLPKGACTGMMAGIPGPHNGAPRGDRDTPGKGEKGDPLGPKGDIGE 82  
OY 98 RGQHPKGEKGYPGI-----PPE---LQIAFMASLATHPSNONGIIFSSVETNIGNF 147  
DB 83 TGVPAEGPRGPGIQRKKEGEGAYVRSFVSGLTYTTPMPLRFTKITYNOQNH 142  
OY 148 EDVMTGRGAPYGVYFFFTSMKHEDEEYVYVLMHNGNTVFSMYSEMKKSDPTSSNH 207  
DB 143 YDGSIGKRFHCNIPGLYFAHYHTVY--MKDVVSLFKKDKAMLFYYDOYQENNVQASGS 200  
OY 208 AVLKAKGDEWLMR-GNG---ALHGDHORESTFAGFLIF 243  
DB 201 VLLHLEVGDDQVWLQYVYGEGERNGLYADNDNDSTFTGFLLY 240

RESULT 8  
US-09-336-536-20  
Sequence 20, Application US/09336536  
Patent No. 6406884  
GENERAL INFORMATION:  
APPLICANT: Leiby, K.  
APPLICANT: McKay, C.  
APPLICANT: Bossone, S.  
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

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      : FILE REFERENCE: 7853-144
      : CURRENT APPLICATION NUMBER: US/09/336,536
      : CURRENT FILING DATE: 1999-06-18
      : NUMBER OF SEQ ID NOS: 75
      : SOFTWARE: PatentIn Ver. 2.0
      : SEQ ID NO 20
      : LENGTH: 244
      : TYPE: PRF
      : ORGANISM: Homo sapiens
US-09-336-536--20

Query Match          21.5%; Score 293.5; DB 4; Length 244;
Best Local Similarity 34.5%; Pred. No. 8.2e-22;
Matches 76; Conservative 35; Mismatches 72; Indels 31; Gaps
9.

QY 53 OGP-----PGPPG-----PGATPNCNNGNNCGATGHEGAKKGGDKD---LGPR---GE 97
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 23 OGPGVLLPLRPKACTGTMMAGTIGHHGNHNPARDGRDGTGPKGEGEDGLTGPKDDIGE 82
    :|: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |

QY 98 RGOHPRKEKGKPGI-----PE-----LQIAFMASLAHFENONSGILFFSEVTNIGNF 147
    :|: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |
Db 83 TGVPAEAPRGRPGITGKRKGERGEGAYYRSASFVGLETVYTTPMNPRIETKIETYNOQH 142
    :|: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |

QY 148 FDVMTRGRCGARPYGVYFTFSMAKHEDVEEVYUULMHNCNTVFMSYSYEMKKSDPTSNH 207
    :|: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |
Db 143 YDGSGTKRHCHNIPGLTYFAHTIVY--MKDVAVSLFKKKKAMLFITYDOYQENNVDASGS 200
    :|: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |

QY 208 AVLKLAKGDEWLRN-GNG---ALHGDRHRETFAGELLE 243
    :|: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |
Db 201 VLLHLEVGDOVWLQYVGEGERNGTLADNDNDSTFGFLTX 240
    :|: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |

RESULT 9
US-09-530-423-1
: Sequence 1, Application US/09530423
: Patent No. 6461821
: GENERAL INFORMATION:
: APPLICANT: Otsuka Pharmaceutical Co., Ltd.
: TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a
: TITLE OF INVENTION: diagnostic method for arteriosclerosis and a kit
: FILE REFERENCE: p98-51
: CURRENT APPLICATION NUMBER: US/09/530,423
: CURRENT FILING DATE: 2000-05-01
: PRIOR APPLICATION NUMBER: JP H9-297569
: PRIOR FILING DATE: 1997-10-29
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 244
: TYPE: PRF
: ORGANISM: Abdominal fat tissue from myoma uteri
US-09-530-423-1

Query Match          21.5%; Score 293.5; DB 4; Length 244;
Best Local Similarity 34.5%; Pred. No. 8.2e-22;
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps
9.

QY 53 OGP-----PGPPG-----PGATPNCNNGNNCGATGHEGAKKGGDKD---LGPR---GE 97
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 23 OGPGVLLPLRPKACTGTMMAGTIGHHGNHNPARDGRDGTGPKGEGEDGLTGPKDDIGE 82
    :|: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |

QY 98 RGOHPRKEKGKPGI-----PE-----LQIAFMASLAHFENONSGILFFSEVTNIGNF 147
    :|: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |
Db 83 TGVPAEAPRGRPGITGKRKGERGEGAYYRSASFVGLETVYTTPMNPRIETKIETYNOQH 142
    :|: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |

QY 148 FDVMTRGRCGARPYGVYFTFSMAKHEDVEEVYUULMHNCNTVFMSYSYEMKKSDPTSNH 207
    :|: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |
Db 143 YDGSGTKRHCHNIPGLTYFAHTIVY--MKDVAVSLFKKKKAMLFITYDOYQENNVDASGS 200
    :|: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |

QY 208 AVLKLAKGDEWLRN-GNG---ALHGDRHRETFAGELLE 243
    :|: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |
Db 201 VLLHLEVGDOVWLQYVGEGERNGTLADNDNDSTFGFLTX 240
    :|: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |: |

```

```

RESULT 10
US-09-140-804-8
; Sequence 8, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-140-804-8

Query Match      21.0%; Score 287; DB 4; Length 247;
Best Local Similarity 31.9%; Pred. No. 3,8e+21;
Matches 82; Conservative 40; Mismatches 101; Indels 34; Gaps 10;

6 LIYWQALAFPLPFCODEYMESPQTGG--LPDCKSCCHGDSFRGYCGPPGPAPPG 63
   :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 2 LLLQLALLFLILIP--SHARDVYTTBELAPALVPKGTCA-----GMMA-----GI PG 48
   :|::||::||::||::||::||::||::||::||::||::||::||::||

Oy 64 IPGNGNNGNNGCATGCEAKGEKGKGLGRGER---GQHCPRKEKCP-----GI PP 114
   ||::||::||::||::||::||::||::||::||::||::||::||::||

Db 49 HPGHGTCRGCRGDSTPEEKCEKGDAGLLPGRGETGVDMGAECPKGFPOTPGRKGEPG 108
   ||::||::||::||::||::||::||::||::||::||::||::||::||

Oy 115 E-----LQIAFMASLATHTFSNONSGIFESSVEETNIGNFVDVMTRGRCVAVSGVFPTFSMM 170
   ::||::||::||::||::||::||::||::||::||::||::||::||::||

Db 109 EAAYVRSAFVSGLGETRYTVPVPIRFRTKIFYNQGNHYDGSGTKRYCNPGLTYFSYHIT 168
   ::||::||::||::||::||::||::||::||::||::||::||::||::||

Oy 171 KHEDVEEYIVYLIMHNGTVTFNSYSTEMKKGSOTSSNAVALKLAKDEYLMRN-GNC---A 226
   ::||::||::||::||::||::||::||::||::||::||::||::||::||

Db 169 VY--MKDVKSLEFFKDKAKVLFTYDOYOKERNVDASGVLLHLEVGDQVWLQYVGDDHGNG 226
   ::||::||::||::||::||::||::||::||::||::||::||::||::||

Oy 227 LGHDHORESTFAGFLF 243
   |::||::||::||::||::||::||::||::||::||::||::||::||::||

Db 227 LYADNVNDSTFTGFLLY 243

RESULT 11
US-09-118-408-3
; Sequence 3, Application US/09118408A
; Patent No. 6265544
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-30
; CURRENT APPLICATION NUMBER: US/09/118,408A
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 60/053,154
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-118-408-3

Query Match      21.0%; Score 287; DB 4; Length 247;
Best Local Similarity 31.9%; Pred. No. 3,8e+21;
Matches 82; Conservative 40; Mismatches 101; Indels 34; Gaps 10;

6 LIYWQALAFPLPFCODEYMESPQTGG--LPDCKSCCHGDSFRGYCGPPGPAPPG 63

```



Db 2 LLLALLFLILP-SHAEDVTTTEELAPALVPPKGTCA-----GMAA-----GIPG 48  
OY 64 IPGNNGNNGNNGATGHEGAKGEGKDGKDLGPRGER---GOGPRGEGKYP-----GIPP 114  
Db 49 HPNGHGTGRGROGTPEKEGKDGAGLLGPKGEGDVMGAGPKGFPOTGPKRKEPG 108  
OY 115 E-----LQAFMASLATHFSNONGSITFSSVETNIGNFDMVTRGFGAPVSGVFFETFSM 170  
Db 109 EAAVYKRSASFVSGLETRVTVNVPNVPFRFKIFYNOONHDSGTGKFCYCNIPGLYFYSHT 168  
OY 171 KHEDEEYVYVLMHNGNTVFSMYEKMKGSDTSSNAVLKLAGDEWLM-KNG---A 226  
Db 169 VY--MKDVKVSILFKDKAVLFTYDQYDEKNVDQASGVLLHLEVGDQWLVQYDGDHNG 226  
OY 227 LHGDHORSTFAGFLIF 243  
Db 227 LYADNVNDSTFTGFLY 243

## RESULT 12

US-09-506-855-3  
Sequence 3, Application US/09506855  
Patent No. 6448221  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Lasser, Gerald W.  
APPLICANT: Bishop, Paul D.  
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND  
FILE REFERENCE: 99-12  
CURRENT APPLICATION NUMBER: US/09/506,855  
CURRENT FILING DATE: 2000-02-17  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 247  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-506-855-3

Query Match 21.0%; Score 287; DB 4; Length 247;  
Best Local Similarity 31.9%; Pred. No. 3.8e-21;  
Matches 82; Conservative 40; Mismatches 101; Indels 34; Gaps 10;  
OY 6 LIYQULALFLPRLCDEYVESQGTG--LPPDCSKCHGDSFRGYQPPGPPGPG 63  
Db 2 LLLALLFLILP-SHAEDVTTTEELAPALVPPKGTCA-----GMAA-----GIPG 48  
OY 64 IPGNNGNNGNNGATGHEGAKGEGKDGKDLGPRGER---GOGPRGEGKYP-----GIPP 114  
Db 49 HPNGHGTGRGROGTPEKEGKDGAGLLGPKGEGDVMGAGPKGFPOTGPKRKEPG 108  
OY 115 E-----LQAFMASLATHFSNONGSITFSSVETNIGNFDMVTRGFGAPVSGVFFETFSM 170  
Db 109 EAAVYKRSASFVSGLETRVTVNVPNVPFRFKIFYNOONHDSGTGKFCYCNIPGLYFYSHT 168  
OY 171 KHEDEEYVYVLMHNGNTVFSMYEKMKGSDTSSNAVLKLAGDEWLM-KNG---A 226  
Db 169 VY--MKDVKVSILFKDKAVLFTYDQYDEKNVDQASGVLLHLEVGDQWLVQYDGDHNG 226  
OY 227 LHGDHORSTFAGFLIF 243  
Db 227 LYADNVNDSTFTGFLY 243

## RESULT 13

US-08-463-911-4  
Sequence 4, Application US/08463911  
Patent No. 5869330  
GENERAL INFORMATION:  
APPLICANT: Scherer, Philipp E.  
APPLICANT: Lodish, Harvey F.

TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED  
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,911  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: WH195-05  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 246 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-463-911-4

Query Match 20.0%; Score 274; DB 2; Length 246;  
Best Local Similarity 31.3%; Pred. No. 7.6e-20;  
Matches 71; Conservative 29; Mismatches 79; Indels 48; Gaps 7;  
OY 51 GYCGPPGPPGPGIPGNGNNGNNGATG-----EGAKGEGKDGKDLGPRERORHGRK 104  
Db 32 GCYGIPGMPGMPGAGKKGKHDGPKGEPGIPAVPGGPGGEGMPGPHRKNR 91  
OY 105 GEGYGPPI-----DELO-----IAFMASLATHFSNONGSITFSSVETNIGNF 147  
Db 92 GTSGLPDPGPPGPPGEGVEBGRYKOKHOSVTVTRÖTTOYEANALVRFNSVVTNPOGH 151  
OY 148 FDMVTRGFGAPVSGVFFETFSMKHEDVEEYVYVLMHNGNTVFSM-----SYEMK 198  
Db 152 YNPSGKFTCEVPLIYERY-----YSHANLCVHLNMLNARVASFCDIHF 198  
OY 199 GKSDTSSNAVLKLAGDEWLMRG--NGALHGDHORSTFAGFLIF 243  
Db 199 NSKOYSSGALLRLRGDEWMLSVNDYNGMV-GIEGSNSVFSGLIF 244

## RESULT 14

US-09-370-838-185  
Sequence 185, Application US/09370838  
Patent No. 6444425  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Mohamath, Rodiah  
APPLICANT: Secrist, Heather  
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF  
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE  
FILE REFERENCE: 210121.475C1  
CURRENT APPLICATION NUMBER: US/09/370,838  
CURRENT FILING DATE: 1999-08-09  
EARLIER APPLICATION NUMBER: US 09/285,323  
EARLIER FILING DATE: 1999-04-02  
NUMBER OF SEQ ID NOS: 289

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 185  
LENGTH: 746  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-370-838-185

Query Match 20.0%; Score 273; DB 4; Length 746;  
Best Local Similarity 29.6%; Pred. No. 4,4e-19;  
Matches 72; Conservative 43; Mismatches 90; Indels 38; Gaps 8;

QY 34 GLPDCSKCCHGDS-----FRGYGPP-----GPPGPGIGPNHNGNN 74  
DB 509 GLP-----SISNGNTSOLQFQAREYSGAPYSQRDNFQOCYKRGSTGCGPRANSRAGMSDSS 564  
QY 75 GATGHEGAKCEKGDGLGPRGERGQ-----HGPKGE---KGYPGIPPELQIAFMAS 123  
DB 565 QVSSPE--RDNETFNSGDSGQDSRSMTPVVDVPTNPATILPVHYV--LPQOMRVAFSA 622  
QY 124 LATIFS--NONGSIISSVEINIGNFDVMTGRGAPYSGVYFTFSMKHEDVEEYVY 181  
DB 623 RTSNLAPGTLDQPIVFDLLNMLGTFDLQGRNCPVNGTYVIFPHMLKLAIVNPLYV 682  
QY 182 LMHNGNTVFSWYSYEMKGSPTSSNHAVLKLAGDEVYLRMGALHGDHQRFTSFAGFL 241  
DB 683 LMKNEVLSAYANDGAPDHETASNAHLLQLFQCDQIWLRLHGAITYSSMKYSTPSGYL 742  
QY 242 LFE 244  
DB 743 LYQ 745

RESULT 15  
US-09-336-536-4  
Sequence 4, Application US/09336536  
Patent No. 6406884  
GENERAL INFORMATION:  
APPLICANT: Leiby, K.  
APPLICANT: McKay, C.  
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
FILE REFERENCE: 7853-144  
CURRENT APPLICATION NUMBER: US/09/336,536  
CURRENT FILING DATE: 1999-06-18  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 228  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-336-536-4

Query Match 19.3%; Score 264.5; DB 4; Length 228;  
Best Local Similarity 32.4%; Pred. No. 6,3e-19;  
Matches 68; Conservative 36; Mismatches 79; Indels 27; Gaps 7;

QY 56 PGPPGPGIPGNHGN-----NGNNGATGHEGAKGEGD-----KGDGPRGERGQ 100  
DB 14 PGHPGLPCTPGHNSQGLPGRGRDGRDGPAGAPCEKEGEGRPGLPGRGDPGPRGEAGP 73  
QY 101 HGPKGEGKGYPIPELQIAFMASLATHSNONGSIISSVEINIGNFDVMTGRGAPYS 160  
DB 74 AGPTGPAGECSVPSPASARSRSRPPPSDAPLPEDRVLVNEDGHAIDAYTGKFTCOV 133  
QY 161 GYVFTFSMKHEDVEEYVY--LMHNGNTVFSWYSYEMKGS--KSDTSSNHAVLKLAGD 216  
DB 134 GYVYFAV-----HATVYRASLDPLVKNGESIASFPQF--FGWPKPASLSGAMVRLERPD 188  
QY 217 EWLRLMGNG--ALHGDHQRFTSFAGFLF 243  
DB 189 QVWVGVGVGDYIGIYASIKTIDSTFSGFLVY 218

Search completed: January 15, 2003, 19:41:37  
Job time : 37 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 15, 2003, 19:33:35 ; Search time 49 Seconds  
(without alignments)

482.634 Million cell updates/sec

Title: US-10-036-041-2

Perfect score: 1367

Sequence: 1 MWMQLIYWLALFLPFC.....LHGDRHRSFPAGFLFETK 246

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description               |
|------------|-------|-------------|--------|-------|---------------------------|
| 1          | 293.5 | 21.5        | 244    | 2     | JC4708 gelatin-binding 28 |
| 2          | 280.5 | 20.5        | 674    | 2     | S23297 collagen alpha 1(X |
| 3          | 278.5 | 20.4        | 680    | 2     | S13216 collagen alpha 1(X |
| 4          | 275   | 20.1        | 674    | 2     | S13301 collagen alpha 1(X |
| 5          | 274   | 20.0        | 246    | 2     | S29328 complement subcomp |
| 6          | 270   | 19.8        | 680    | 1     | CGH01D collagen alpha 1(X |
| 7          | 264.5 | 19.3        | 219    | 2     | T14782 hypothetical prote |
| 8          | 258.5 | 18.9        | 744    | 1     | A34246 collagen alpha 1(X |
| 9          | 256.5 | 18.8        | 744    | 2     | S15435 collagen alpha 1(X |
| 10         | 255   | 18.7        | 245    | 1     | CIH00C complement subcomp |
| 11         | 251.5 | 18.4        | 253    | 1     | CIH00B complement subcomp |
| 12         | 251.5 | 18.4        | 744    | 1     | S23298 collagen alpha 1(X |
| 13         | 249   | 18.2        | 635    | 2     | A57131 collagen alpha 2(X |
| 14         | 239.5 | 18.1        | 743    | 1     | S23779 collagen alpha 1(X |
| 15         | 239.5 | 17.5        | 245    | 2     | S19018 complement subcomp |
| 16         | 236.5 | 17.3        | 253    | 2     | S49158 complement protein |
| 17         | 231.5 | 16.9        | 253    | 2     | I49560 complement C1q B C |
| 18         | 226   | 16.5        | 423    | 2     | A55797 collagen precursor |
| 19         | 219   | 16.0        | 245    | 1     | CIH00A complement subcomp |
| 20         | 216   | 15.8        | 920    | 2     | A45748 collagen alpha 1(X |
| 21         | 215   | 15.7        | 992    | 2     | T08772 hypothetical prote |
| 22         | 211.5 | 15.5        | 366    | 2     | S11449 collagen short cha |
| 23         | 210.5 | 15.4        | 423    | 2     | A41207 collagen 13, nonfi |
| 24         | 208   | 15.2        | 2944   | 2     | A54849 collagen alpha 1(X |
| 25         | 207.5 | 15.2        | 775    | 2     | A61228 collagen alpha 2(X |
| 26         | 207.5 | 15.2        | 1349   | 2     | I46103 type VII collagen  |
| 27         | 203.5 | 14.9        | 1707   | 2     | A33526 collagen alpha 2(X |
| 28         | 203.5 | 14.9        | 1712   | 1     | CGH02B collagen alpha 2(X |
| 29         | 202   | 14.8        | 215    | 2     | B48150 hibernation-relate |

|    |       |      |      |   |                           |
|----|-------|------|------|---|---------------------------|
| 30 | 201   | 14.7 | 215  | 2 | C48150 hibernation-relate |
| 31 | 197   | 14.4 | 171  | 2 | A34493 collagen alpha 1(X |
| 32 | 196   | 14.3 | 224  | 2 | A60032 cerebellin-like (X |
| 33 | 195.5 | 14.3 | 1315 | 2 | collagen alpha 1(X        |
| 34 | 195.5 | 14.3 | 1774 | 2 | collagen alpha 1(X        |
| 35 | 193.5 | 14.2 | 1744 | 2 | S40991 collagen alpha 1(X |
| 36 | 193   | 14.1 | 296  | 2 | A31219 collagen 1 - Caeno |
| 37 | 193   | 14.1 | 301  | 2 | T21314 hypothetical prote |
| 38 | 192.5 | 14.1 | 921  | 2 | S42617 collagen alpha 1(X |
| 39 | 192   | 14.0 | 1466 | 1 | CGH07L collagen alpha 1(X |
| 40 | 190.5 | 13.9 | 289  | 2 | T26812 hypothetical prote |
| 41 | 189   | 13.8 | 193  | 2 | A37873 cerebellin precus  |
| 42 | 189   | 13.8 | 375  | 1 | A45225 pulmonary surfacta |
| 43 | 189   | 13.8 | 1464 | 2 | S59856 collagen alpha 1(X |
| 44 | 187.5 | 13.7 | 921  | 2 | S40495 collagen alpha 1(X |
| 45 | 187   | 13.7 | 684  | 2 | A53019 collagen alpha 1(X |

## ALIGNMENTS

```
RESULT 1
JC4708
gelatin-binding 28K protein precursor - human
N:Alternate names: adipose specific collagen-like factor
C:Species: Homo sapiens (man)
C:Date: 10-May-1996 #sequence
C:Accession: J04708; J04944
R:Maeda, K.; Okubo, K.; Shimomura, I.; Funahashi, T.; Matsuzawa, Y.; Matsubara, K.
Biochem. Biophys. Res. Commun. 221, 286-289, 1996
A:Title: cDNA cloning and expression of a novel adipose specific collagen-like factor
A:Reference number: J04708; MUID:96224171; PMID:8619847
A:Accession: J04708
A:Molecule type: mRNA
A:Residues: 1-244 <NAE>
A:Cross-references: DBJ:D45371; MID:9871886; PIDN:BA08227.1; PID:9871887
A:Experimental source: adipose tissue
R:Nakano, Y.; Tohe, T.; Choi-Miura, N.H.; Mazda, T.; Tomita, M.
J. Biochem. 120, 803-812, 1996
A:Title: Isolation and characterization of GPR28, a novel gelatin-binding protein pur
A:Reference number: J04944; MUID:97103474; PMID:8947845
A:Accession: J04944
A:Molecule type: protein
A:Residues: 19-38;93-100;101-112;135-149;173-178 <NAK>
C:Comment: This protein is an endogenous factor that binds with a collagen-like domai
C:Genetics:
A:Gene: apm1
C:Superfamily: unassigned collagens; complement C1q carboxyl-terminal homology
C:Keywords: adipose tissue; glycoprotein; hydroxyproline
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-244/Product: gelatin-binding 28kDa protein #status experimental <MAT>
F:42-107/Region: collagen-like
F:114-241/Domain: complement C1q carboxyl-terminal homology <C1Q>
F:95/Modified site: 4-hydroxyproline (Pro) #status experimental
F:230/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      21.5%  Score 293.5  DB 2;  Length 244;
Best Local Similarity 34.5%  Pred. No. 7e-17; 78;  Indels 31;  Gaps 9;
Matches 76;  Conservative 35;  Mismatches 31;

OY 53 OGP-----PGPPG-----PGIPGNHNGNNGATGHEGAKGKGDGD--LQPR--GE 97
    111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 23 QGEGVLLPLPKGACCTGMMAGITPHPHNGNAPGHDGDTGFGKGEKGDPELLPKDGICE 82
    111 111 111 111 111 111 111 111 111 111 111 111 111 111
OY 98 RGOHGRKGEKGYPGI-----PPE-----LQIAFMASLATHFSNONGIIFSSVETNIGNF 147
    111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 83 TGVPGAGEGFRGEPGIGCRKCEPGEAGYVRSAPSVLETFVTIPNMPIRTKTFYMOQNH 142
    111 111 111 111 111 111 111 111 111 111 111 111 111 111
OY 148 FDMTGRFGAPVSGVYFFTFSSMKKHEDVEVYVYLMHNGTFSVSMYSYEKKGSDSSNH 207
    111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 143 YDSSTGRFHCNIPGLYFAHITVY--MKDVKVSLEKRRKRAFLFTDQYQENNVDAQSSG 200
    111 111 111 111 111 111 111 111 111 111 111 111 111 111
OY 208 AVLKAKGDEWLMR-GNG--ALHGDRHRSFPAGFLFETK 243
```

DB 201 VLLHLEVGDDQWVLGYGGEGERNGLYADNDNDSTFGFLLY 240

RESULT 2

S23297

collagen alpha 1(X) chain precursor - chicken

N:Alternate names: type X collagen

C:Species: Gallus gallus (chicken)

C:Date: 07-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 13-Aug-1999

C:Accession: S23297; A31896; S65594; S77711; I50218

R:Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.; Mochizuki, N.; Olsen, B.R.

A:Title: The molecular biology of collagens with short triple-helical domains.

A:Reference number: S22243

A:Accession: S23297

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-674 <NIN>

R:LuValle, P.; Ninomiya, Y.; Rosenblum, N.D.; Olsen, B.R.

J. Biol. Chem. 263, 18378-18385, 1988

A:Title: The type X collagen gene, intron sequences split the 5'-untranslated region and

A:Reference number: A31896; MUID:89054019; PMID:2461368

A:Accession: A31896

A:Molecule type: mRNA

A:Residues: 1-75 <LUV>

R:Ninomiya, Y.; Gordon, M.; van der Rest, M.; Schmid, T.; Linsenmayer, T.; Olsen, B.R.

J. Biol. Chem. 261, 5041-5050, 1986

A:Title: The developmentally regulated type X collagen gene contains a long open reading

A:Reference number: I50218; MUID:86168227; PMID:3082876

A:Accession: S65594

A:Molecule type: DNA

A:Residues: 'T', '9', 'D', '11-12', 'EDQMKLYLEFTW', '30-31', 'TCKSGRAFTYMILONWADLVSSHT', '48-89', 'L', '629', 'PQAVLSIKSRITKCGSSCOIOPMVSIPLNMFILISOVYLSKNINPIETWS' <NIN>

A:Cross-references: EMBL:M31496; NID:9211699; PIDN:AAA48736.1; PID:9211700

A:Accession: S77711

A:Molecule type: protein

A:Residues: 104-112, 'X', '114-117, 453-466 <NIN2>

C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology

C:Keywords: coll; coll; extracellular matrix; glycoprotein; homotrimer; hydroxyproline

F:1-18/Domain: signal sequence #status predicted <SIG>

F:547-673/Domain: complement C1q carboxyl-terminal homology <C1Q>

F:453,456/Modified site: hydroxyproline (Pro) #status experimental

F:611/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.5%; Score 280.5; DB 2; Length 674;

Best Local Similarity 30.9%; Pred. No. 2,3-15;

Matches 76; Conservative 23; Mismatches 90; Indels 57; Gaps 5;

QY 51 GYGRPRGPRGPRGIRGNGNNGNNGATGHEGAKGEG-----DKDDLGRGREG 99

DB 427 GINERPRGGRSGIPGIRGIRGPRGMPGAPGAGAPGLPRGATKGLRGPMGPRG 486

QY 100 OHGPRGEGKYGIP-----PELOI----- 118

DB 487 PRGRGNGSGRGLRPRPRPRPGOSTIRPEGYVNGESNELSGSMFKAGANQALTMGPRV 546

QY 119 AFMASLATHESNONGSILFFSVETNIGNFEDVMTGRGAPVSGYVFTFSMKKEDVEEV 178

DB 547 AFTVLISKAYGATVPIDFKRLILYRQOHYDPRGIFCRIPGLYEFYHY--HAKGTN 604

QY 179 VYVLMHNTQFESMYEMKGRKSDTSSNHAVLAKAGDEVLLRGN---GALHGDHQFES 235

DB 605 WALKTKNSPVWYTYDEYQKILDOASGSAVIDLMENDQWVLOLRNSENGLYSESYVHS 664

QY 236 TFAGFL 241

DB 665 SFSGFL 670

RESULT 3

S31216

```

collagen alpha 1(X) chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text-change 13-Aug-1999
C:Citation: S31216: S28807; S22215; S30127; I48299; S26397; S31830
R:Kong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M.E.
Eur. J. Biochem. 213, 99-111, 1993
A>Title: Intron-exon structure, alternative use of promoter and expression of the mouse
A:Reference number: S31216; MUID:93238750; PMID:8477738
A:Accession: S31216
A:Molecule type: DNA
A:Residues: 1-680 <KON>
A:Cross-references: EMBL:X621610; NID:949793; PIDN:CAAA79736.1; PID:949794
R:Elima, K.; Berola, I.; Rosati, R.; Metsaerant, M.; Garofalo, S.; de
Biochem. J. 289, 247-253, 1993
A>Title: The mouse collagen X gene: complete nucleotide sequence, exon structure and
A:Reference number: S28807; MUID:93143676; PMID:8424763
A:Accession: S28807
A:Molecule type: DNA
A:Residues: 1-285,'A',287-680 <ELI>
A:Cross-references: EMBL:X67348; NID:950480; PIDN:CAAA7763.1; PID:950481
R:Elima, K.; Metsaerant, M.; Kallio, J.; Peraelae, M.; Berola, I.; Garofalo, S.; de
Biochim. Biophys. Acta 1130, 78-80, 1992
A>Title: Specific hybridization probes for mouse alpha-2(I) and alpha-1(X) collagen
A:Reference number: S22215; MUID:92182017; PMID:1543731
A:Accession: S22215
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 385-450,'K',452-627 <ELA>
A:Cross-references: EMBL:X63013; NID:949795; PIDN:CAAA4741.1; PID:949796
R:Appe, S.S.; Olsen, B.R.
Matrix 13, 165-179, 1993
A>Title: Characterization of the mouse type X collagen gene.
A:Reference number: S30127; MUID:93261348; PMID:8492743
A:Accession: S30127
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12,'F',14-26,'S',28-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499
R:Appe, S.S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R.
Eur. J. Biochem. 206, 217-224, 1992
A>Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse
A:Reference number: I48299; MUID:92267014; PMID:1587271
A:Accession: I48299
A>Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 52-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566,'C',566-680
A:Cross-references: EMBL:X65121; NID:950482; PIDN:CAAA6237.1; PID:9667031
R:Summers, T.A.; Irwin, M.H.; Mayne, R.; Ballan, G.
J. Biol. Chem. 263, 581-587, 1988
A>Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an anti-
A:Reference number: S26397; MUID:88087150; PMID:2826450
A:Accession: S26397
A:Molecule type: protein
A:Residues: 'SDGYFSQ',24-26,'KQ' <SUM>
C:Genetics:
A:Gene: Coll10a-1
A:Map position: 10
A:Introns: 51/3
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C:Keywords: coll; extracellular matrix; glycoprotein; homotrimer
F:1-18/Domains: signal sequence #status predicted <IG>
F:19-680/Product: collagen alpha 1(X) chain #status predicted <MNT>
F:553-679/Domains: complement C1q carboxyl-terminal homology <CIQ>

Query Match 20.4%; Score 278.5; DB 2; Length 680;
Best Local Similarity 30.5%; Pred. No. 3.4e-15;
Matches 73; Conservativity 34; Mismatches 87; Indels 45; Gaps 7;

45 GDYSRGVGGPGRPGPGIPGNGNNGNNGATG-----HGAKGKGDKDLGPRERG 99
db 443 GEGTIPGRGPGPGPGVGFGRFOSKDPGPGAGATGATGLNGPTGPPPPRGHSG 502
100 QHGPGRGKGVGPDP-----PELQ-----IAPMASLATHF 128

```



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pe Schmid.
A:Reference number: 151870; MUID:94136476; PMID:8304336
A:Accession: 151870
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 520-597; 'D', 599-680 <MAL>
A:Cross-references: GB:S66531; NID:9545180; PID:NAC60615.1; PID:9545181
A:Note: mutant sequence from patient with metaphyseal chondrodysplasia type Schmid
C:Note: a second mutant sequence with 614-pro is also described
C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit
ed and subsequently O-glycosylated.
C:Genetics:
A:Gene: GDB:COL10A1
A:Cross-references: GDB:128635; OMIM:120110
A:Map position: 6q21-q22
A:Introns: 52/1
A:Note: a defect in this gene may cause Schmid metaphyseal chondrodysplasia
C:Complex: type X collagen may be a homotrimer
C:Function:
A:Description: structural component of extracellular fibrous polymer specifically and th
be important for skeletogenesis
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C:Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxylysine;
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
F:19-56/Domain: amino-terminal nonhelical #status predicted <NC2>
F:57-519/Region: interrupted helical
F:520-680/Domain: amino-terminal nonhelical #status predicted <NC1>
F:553-679/Domain: complement C1q carboxyl-terminal homology <C1Q>
F:617/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          19.8%; Score 270; DB 1; Length 680;
Best Local Similarity 28.5%; Pred. No. 1.7e-14;
Matches 75; Conservative 28; Mismatches 102; Indels 58; Gaps 6;

QY 34 GLPPDCSKCHGDSYFRGYPGPPGPIPGNHGNGNGATGHEGAKGEKD----- 88
DB 419 GLRPGPR- -GAKGPHNGENGAPRGAPGIPGTRPIGPIGPGSGDPCSGPPG 476
QY 89 -----KGLDGRGERGQHGPRGEGKYPGIP-----PELQ- 117
DB 477 PAGIATKGLNGPGRGPPRGHSGEPGLPGRPPGQAVMPEGFIKAGQPSLSG 536
QY 118 -----IAFMASLATHFSNONGSIIFSSVETNIGNFEDVMTGRGCAVSGV 162
DB 537 TPLVANSQGVCTGMPASFTVLISKAYPAIGTPIPFDKILYNRQHYDPRFTGICQIPGI 596
QY 163 YFTFESMKHEDVEEYVYLMHNGNTVFSMYSEMKGSDTSSNHAVLAKGDEYWLRM 222
DB 597 YFESYIV--HVKGNHWAVLYLNKGTPTVMTYDEYTKGILDQASGSAIIDLTDNDYWLQ 654
QY 223 GN--GALHGDNHQRSTFAGFL 242
DB 655 PNAESNGLYSSEYVHSSFGFLV 677

RESULT 7
T14782
hypothetical protein DKFZp586B0621.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000
C:Accession: T14782
R:Ottewill, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, August 1999
A:Reference number: 218184
A:Accession: T14782
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <OTY>
A:Cross-references: EMBL:AL110261
A:Experimental source: adult uterus; clone DKFZp586B0621
C:Genetics:
A:Note: DKFZp586B0621.1.

```

```

C:Superfamily: complement C1q carboxyl-terminal homology

Query Match          19.3%; Score 264.5; DB 2; Length 219;
Best Local Similarity 32.4%; Pred. No. 1.5e-14;
Matches 68; Conservative 36; Mismatches 79; Indels 27; Gaps 7;

QY 56 PGRPPGPIGNGN-----KGNNGATGHEGAKGEKD-----KGLDGRREKQ 100
DB 5 PGRHGLGRTGTHGSQLPGRDRDRDAPGAPGEGGGRGLGPRGDPGRGEAP 64
QY 101 HGRGKEGYGIPPELOIAFMASLATHFSNONGSIIFSSVETNIGNFEPVMTGRGAPVS 160
DB 65 AGPTGAGGCSYPRRSFSAKRSRVPSPDAPLPFDRLVNVGCHYAVTKFTCYRP 124
QY 161 GYVFTFESMKHEDVEEYVY--LMHNGTVFSMYSEMKG--KSDTSSNHAVLAKGD 216
DB 125 GYVYFVAV---HATVYRASLPQDLVKNGESISFFQF--FGGWPKPASLSGAWVRLEPD 179
QY 217 EYVLRMGNG---ALHGDHQRSTFAGFL 243
DB 180 QVWVQVGVGDYIGIYASIKDTSTFSGFLV 209

RESULT 8
A34246
collagen alpha 1(VIII) chain precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A34246
R:Yamaguchi, N.; Benay, P.D.; van der Rest, M.; Nioomiya, Y.
J. Biol. Chem. 264, 16022-16029, 1989
A:Title: The cloning and sequencing of alpha1(VIII) collagen cDNAs demonstrate that t
omins similar to those of type X collagen.
A:Reference number: A34246; MUID:89380199; PMID:2476437
A:Accession: A34246
A:Molecule type: mRNA
A:Residues: 1-744 <YAM>
A:Cross-references: GB:J05042; NID:9164895; PID:AAA31204.1; PID:9164896
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>
F:21-117/Region: amino-terminal nonhelical
F:118-571/Region: interrupted helical
F:572-744/Region: carboxyl-terminal nonhelical
F:617-743/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match          18.9%; Score 258.5; DB 1; Length 744;
Best Local Similarity 30.3%; Pred. No. 1.7e-13;
Matches 79; Conservative 24; Mismatches 103; Indels 55; Gaps 6;

QY 34 GLPPDCSKCHGDSYFRGYPGPPGPIPGNHGNGNGATGHEGA-----KGE 85
DB 486 GLPGD--QGLOGPPGIPGITGPGIPGPKGEPGLPGRPPGVAKGPAVLHGP 543
QY 86 KDKKDLGPRGERGQHGPRGEGKYPGIP-----PELQ- 118
DB 544 PGRGALGPGQGLPGRPPGPPGPAVMPPTPAPDGEYLPDMGLGIDGVKTPAYVA 603
QY 119 -----AFMASLATHFSNONGSIIFSSVETNIGNFEDVMTGRGCAVSGV 165
DB 604 KRKNGGPRAYEMAFYALTAFTLPPGAPRIKPRRLLYNKRQNTNPOTGTGTCVPPVYTF 663
QY 166 TFSMKHEDVEEYVYLMHNGNTVFSMYSEMKGSDTSSNHAVLAKGDEYWLRMGN- 224
DB 664 AYHV--HCKGNVWVALFKNNEPVMTYDEYKGFIDQASGSAVILLRRGDRVFLQMPSE 721
QY 225 --GALHGDNHQRSTFAGFL 243
DB 722 QAAGLYAGQYVHSSFGFLY 742

RESULT 9
S15435

```









GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 15, 2003, 18:56:40 ; Search time 38 Seconds

(without alignments)  
268,505 Million cell updates/sec

Title: US-10-036-041-2

Perfect score: 1367  
Sequence: 1 MLMQLYVQLLFLFLPFC.....LHGDRPSPAGFLFETK 246

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 1367  | 100.0       | 246    | 1     | COT3_HUMAN  |
| 2          | 315   | 23.0        | 289    | 1     | COT7_HUMAN  |
| 3          | 304   | 22.2        | 285    | 1     | COT2_HUMAN  |
| 4          | 297.5 | 21.8        | 258    | 1     | C1RF_HUMAN  |
| 5          | 297.5 | 21.8        | 258    | 1     | C1RF_MOUSE  |
| 6          | 294   | 21.5        | 247    | 1     | APM1_MOUSE  |
| 7          | 293.5 | 21.5        | 244    | 1     | APM1_HUMAN  |
| 8          | 289.5 | 21.2        | 278    | 1     | COT6_HUMAN  |
| 9          | 285.5 | 20.9        | 255    | 1     | GLIC_MOUSE  |
| 10         | 280.5 | 20.5        | 674    | 1     | CA1A_CHICK  |
| 11         | 278.5 | 20.4        | 680    | 1     | CA1A_MOUSE  |
| 12         | 275   | 20.1        | 674    | 1     | CA1A_BOVIN  |
| 13         | 274   | 20.0        | 246    | 1     | C1OC_MOUSE  |
| 14         | 270   | 19.8        | 680    | 1     | CA1A_HUMAN  |
| 15         | 264.5 | 19.3        | 243    | 1     | COT5_HUMAN  |
| 16         | 258.5 | 18.9        | 744    | 1     | CA18_RABIT  |
| 17         | 257.5 | 18.8        | 744    | 1     | CA18_HUMAN  |
| 18         | 257   | 18.8        | 743    | 1     | CA18_MOUSE  |
| 19         | 255   | 18.7        | 245    | 1     | C1OC_HUMAN  |
| 20         | 254   | 18.6        | 419    | 1     | COLE_MOUSE  |
| 21         | 251.5 | 18.4        | 251    | 1     | COLE_MOUSE  |
| 22         | 249   | 18.2        | 635    | 1     | CA28_HUMAN  |
| 23         | 239.5 | 17.5        | 245    | 1     | C1OA_MOUSE  |
| 24         | 236.5 | 17.3        | 253    | 1     | C1OB_MOUSE  |
| 25         | 231.5 | 16.9        | 253    | 1     | C1OB_MOUSE  |
| 26         | 226   | 16.5        | 281    | 1     | COT1_HUMAN  |
| 27         | 219   | 16.0        | 245    | 1     | C1OA_HUMAN  |
| 28         | 211.5 | 15.5        | 366    | 1     | CAS4_EPHMU  |
| 29         | 208   | 15.2        | 2944   | 1     | CA17_HUMAN  |
| 30         | 203.5 | 14.9        | 1707   | 1     | CA24_MOUSE  |
| 31         | 203.5 | 14.9        | 1712   | 1     | CA24_HUMAN  |
| 32         | 202   | 14.8        | 215    | 1     | HP25_TAMSI  |
| 33         | 201   | 14.7        | 215    | 1     | HP27_TAMSI  |

|    |       |      |      |   |            |                    |
|----|-------|------|------|---|------------|--------------------|
| 34 | 200   | 14.6 | 1516 | 1 | CA1H_HUMAN | P39060 homo sapien |
| 35 | 196   | 14.3 | 224  | 1 | CERL_RAT   | P98087 rattus norv |
| 36 | 195.5 | 14.3 | 1527 | 1 | CA1H_MOUSE | P39061 mus musculu |
| 37 | 195   | 14.2 | 458  | 1 | COLO_RAT   | O35167 rattus norv |
| 38 | 193.5 | 14.2 | 1758 | 1 | CA1A_CAEL  | P17139 caenorhabd  |
| 39 | 193   | 14.1 | 296  | 1 | CCO1_CAEL  | P08124 caenorhabd  |
| 40 | 193   | 14.1 | 456  | 1 | COLO_HUMAN | O9215 homo sapien  |
| 41 | 192   | 14.0 | 1466 | 1 | CA13_HUMAN | P02461 homo sapien |
| 42 | 189   | 13.8 | 193  | 1 | CERB_HUMAN | P23435 homo sapien |
| 43 | 189   | 13.8 | 193  | 1 | CERB_MOUSE | O9171 mus musculu  |
| 44 | 189   | 13.8 | 375  | 1 | PSPD_HUMAN | P35247 homo sapien |
| 45 | 189   | 13.8 | 1464 | 1 | CA13_MOUSE | P08121 mus musculu |

## ALIGNMENTS

RESULT 1  
COT3\_HUMAN STANDARD: PRT: 246 AA.  
AC O9BXJ4; O96KY1:  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Complement-c1q tumor necrosis factor-related protein 3 precursor  
DE (Secretory protein COR526).  
GN C1QTNF3 OR CTRP3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Piddington C.S., Bishop P.;  
RT "Homo sapiens complement-c1q tumor necrosis factor-related protein.";  
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Maeda T., Hayashi A., Saito T.;  
RT "Molecular cloning, chromosomal localization, and genomic structure of  
RT the human COR526 gene.";  
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 121-246 FROM N.A.  
RA TISSUE=Placenta;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.  
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CC  
CC EMBL: AF329837; AAK17961.1; -  
CC EMBL: AF329876; AAK70344.1; -  
CC EMBL: BC016021; AAH16021.1; -  
CC Genew: HGNC:14326; C1QTNF3.  
CC InterPro: IPR001073; C1Q.  
CC InterPro: IPR000087; Collagen.  
CC Pfam: PF00386; C1q; 1.  
CC Pfam: PF01391; Collagen; 1.  
CC PRINTS: PR00007; COMPLEMENTC1Q.  
CC SMART: SM00110; C1Q; 1.  
CC PROSITE: PS01113; C1Q; 1.  
CC Collagen; signal.  
FT SIGNAL 1 22  
FT CHAIN 23 246  
FT POTENTIAL.  
FT RELATED PROTEIN 3.  
FT

FT DOMAIN 51 113 COLLAGEN-LIKE.  
 FT DOMAIN 114 246 C1Q.  
 FT CONFLICT 214 214 K -> E (LN REF. 3).  
 SQ SEQUENCE 246 AA: 26994 MW: C389B6C3A73E5D29 CRC64;  
 Query Match  
 Best Local Similarity 100.0%; Score 1367; DB 1; Length 246;  
 Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMROLYIQLALFLPCLCODEYMESPQTGGLPPDCSKCHGDSYRGTGPGPPG 60  
 DB 1 MIMROLYIQLALFLPCLCODEYMESPQTGGLPPDCSKCHGDSYRGTGPGPPG 60  
 QY 61 PGELPENNNGNNGATGHEGAKGEGKDGDLGPRGREGQHPKGGKGPGLPELQIAF 120  
 DB 61 PGELPENNNGNNGATGHEGAKGEGKDGDLGPRGREGQHPKGGKGPGLPELQIAF 120  
 QY 121 MASLATHFNSNGSGLIFSSVETNIGNFPDVMGTREGAPVSGYFFTFSMKHEDEVYEV 180  
 DB 121 MASLATHFNSNGSGLIFSSVETNIGNFPDVMGTREGAPVSGYFFTFSMKHEDEVYEV 180  
 QY 181 YLMHNGNTVFSYSTEEMKCKSDTSSNHAVLKLAKGDEVLMRGNGALHGDHORESTFAGF 240  
 DB 181 YLMHNGNTVFSYSTEEMKCKSDTSSNHAVLKLAKGDEVLMRGNGALHGDHORESTFAGF 240  
 QY 241 LLEETK 246  
 DB 241 LLEETK 246

RESULT 2  
 COT7\_HUMAN STANDARD; PRT: 289 AA.  
 ID COT7\_HUMAN  
 AC 09BXJ2;  
 DT 15-JUN-2002 (rel. 41, Created)  
 DT 15-JUN-2002 (rel. 41, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE Complement-c1q tumor necrosis factor-related protein 7 precursor.  
 GN C1QTNF7 OR CTRP7.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Piddington C.S., Sheppard P.O., Bishop P., Lasser G.W.;  
 RT "Homo sapiens complement-c1q tumor necrosis factor-related protein.";  
 RN Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.  
 RC TISSUE-Testis;  
 RA Strausberg R.;  
 RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.  
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DR EMBL: AF329839; AKI1963.1;  
 DR EMBL: BC022187; AAH22187.1;  
 DR Genew: HGNC:14342; C1QTNF7.  
 DR InterPro: IPR001073; C1q.  
 DR InterPro: IPR000087; Collagen.  
 DR Pfam: PF00386; C1q; 1.  
 DR Pfam: PF01391; Collagen; 2.  
 DR PRINTS: PRO0007; COMPLEMENTC1Q.  
 DR SMART: SM00110; C1Q; 1.

DR PROSITE: PS01113; C1Q; 1.  
 KW Collagen; Signal.  
 FT SIGNAL 1 16  
 FT CHAIN 17 289  
 FT DOMAIN 38 139  
 FT DOMAIN 141 276  
 SQ SEQUENCE 289 AA: 30683 MW: A61609FF8D26946 CRC64;  
 Query Match  
 Best Local Similarity 23.0%; Score 315; DB 1; Length 289;  
 Matches 86; Conservative 32; Mismatches 96; Indels 72; Gaps 9;

QY 14 LFLPPLCLCODEYMESPQTGGLPPDCSKCHGDSYRGTGPGPPGPPGPPGHNNGN 73  
 DB 5 LKVTSPALICASGPRGNQLKGENYSPRYIC---SLPGLGPPGPPGPPGPPGPPGPPG 60  
 QY 74 NCATGHEGAKGEGKDGDLGPRGREGQHPKGGKGPGLPELQIAF 103  
 DB 61 PGMDGRDGRKRGKGGKGTAGLRGTGPLGLAGKGGOGGTGKGPGLGREGKEVEYRIGP 120  
 QY 104 -----KGEKYPGIDP-----ELQIAFMASLATHFNSNGSGLIFSSVETNIGNFPDV 150  
 DB 121 PGKRGDRGEGDGLGVCRCGSLVLSAFVSGITTSYPERLPIIFNKVLFGEGEHYNP 180  
 QY 151 MGRFGAPVSGYFFTFEFSNM---KHEDVEYVYLMHNGNTVFSYSTEEMK-----CKS 201  
 DB 181 ATGKFCICAPPGIYFSDYITLANKH-----LAIGLVHNG-----QYRKTFDANTGNH 228  
 QY 202 DTSSNHAVLKLAKGDEVLMRGNGALHGDHORESTFAGFLP 243  
 DB 229 DVASGSTVIYLOPEDEVLMELFTTDONGLEFSDGRMDSLFSGLTLX 274

RESULT 3  
 COT2\_HUMAN STANDARD; PRT: 285 AA.  
 ID COT2\_HUMAN  
 AC 09BXJ5;  
 DT 15-JUN-2002 (rel. 41, Created)  
 DT 15-JUN-2002 (rel. 41, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE Complement-c1q tumor necrosis factor-related protein 2 precursor.  
 GN C1QTNF2 OR CTRP2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Piddington C.S., Bishop P.;  
 RT "Homo sapiens complement-c1q tumor necrosis factor-related protein.";  
 RN Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.  
 RC TISSUE-Muscle;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.  
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DR EMBL: AF329836; AKI1960.1;  
 DR EMBL: BC011699; AAH11699.1;  
 DR Genew: HGNC:14325; C1QTNF2.  
 DR InterPro: IPR001073; C1q.  
 DR InterPro: IPR000087; Collagen.

```

DR Pfam; PF00386; Clq; 1.
DR Pfam; PF01391; Collagen; 2.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR SMART; SM00110; C1Q; 1.
DR PROSITE; PS01113; C1Q; 1.
KM Collagen; Signal.
FT SIGNAL 1 15
FT CHAIN 16 285
FT DOMAIN 40 141
FT DOMAIN 143 285
SQ SEQUENCE 285 AA; 29952 MW; 7E31FF9868D4EDFA CRC64;

Query Match
Best Local Similarity 22.2%; Score 304; DB 1; Length 285;
Matches 73; Conservative 42; Mismatches 74; Indels 58; Gaps 9;

OY 48 SFRGQGPFGPPPP-----GIP---GNHGNNNGATGHEGAKGKDKDGLPR 95
DB 37 SLPGPGPPGPGAPGAPSGMGMGRGKGGKGGGLPGSCSGSGHTKSAFSAV 96
OY 96 GER-----GOHGPKGKGYPGIP-----PELQIAFMASL 124
DB 97 GKAGALGAPGPGKGVNTPGKGTGPKGKGGKGGGLPGSCSGSGHTKSAFSAV 156
OY 125 ATHESSNNGIIFSSVETNIGNFEDVMTGRGAPYSGVYFFTFSSM---KHEDVEEYVY 181
DB 157 TKSYPRELPIKFKDKILMNEGHNASSGKFCVPGIYFYITDITLANKH-----LAIG 211
OY 182 LMHNGNTVFSYSTEEMK-GKSDTSSNAVLKAKGDEVLMR-----GNCALGHDRPST 236
DB 212 LVHNGQ--YRIRTDANGNHDAVSGSTILAKGDEVWLQIFVSEONGLEFYDPYWTDSL 269
OY 237 PAGFLIF 243
DB 270 FTGFLIF 276

RESULT 4
C1RF_HUMAN STANDARD; PRT; 258 AA.
ID C1RF_HUMAN
AC 075973;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C1q-related factor precursor.
GN C1QRF OR CRF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=99097006; PubMed=9878755;
RX Berube N.G., Swanson X.H., Berttram M.J., Kittle J.D., Didenko V.,
RA Baekin D.S., Smith J.R., Pereira-Smith O.M.;
RT "Cloning and characterization of CRF, a novel C1q-related factor,
RT expressed in areas of the brain involved in motor function.";
RL Brain Res. Mol. Brain Res. 63:233-240(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL TISSUE=Placenta;
RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAINSTEM.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.

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CC -----
DR EMBL; AF095154; AAC64186.1; -
DR EMBL; AF410771; AAK95248.1; -
DR EMBL; BC008798; AAH08798.1; -
DR InterPro; IPR001073; Clqagen.
DR InterPro; IPR000087; Collagen.
DR Pfam; PF00386; Clq; 1.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR SMART; SM00110; C1Q; 1.
DR PROSITE; PS01113; C1Q; 1.
KM Collagen; Signal.
FT SIGNAL 1 16
FT CHAIN 17 258
FT DOMAIN 67 115
FT DOMAIN 123 258
SQ SEQUENCE 258 AA; 26452 MW; 52C51CDF59CAE2BF CRC64;

Query Match
Best Local Similarity 21.8%; Score 297.5; DB 1; Length 258;
Matches 76; Conservative 32; Mismatches 89; Indels 25; Gaps 8;

OY 29 SPQSGLEPPDCKSCCHGDSYFRGQGPFGPPGPGIPGHNHNGNNGATGHEGAKGKCD 88
DB 53 SQSGAPPP--STLVQGPQKPGRTKGPDPGPPGPP-----GPPGVPGPGEKKE 101
OY 89 KGDLPGRG--ERQHGPKGKGYPGIPPELQIAFMASLATHSSNONG---IIFSSVETN 143
DB 102 PKPGPPGLPGAGSGGALSTATTITVP---RVAFYAGL-----KNPHEGYEVLFDDVYTN 154
OY 144 IGNFEDVMTGRGAPYSGVYFFTFSS-MKHEDVEEYVYLMHNGNTVFSYSTEEMKSD 202
DB 155 LGNNVDAASGKFTCNIPGYFFTYHVMKGGCTGSMWMDLCKNGVRSALINQDADQNVND 214
OY 203 TSSNNAVLKAKGDEVLMRNGALH-GDHQRPSTFAGFLIF 243
DB 215 YASNSVILHLDAGDEVFIKLDGKAHAGNSNRYSTFSGFTIY 256

RESULT 5
C1RF_MOUSE STANDARD; PRT; 258 AA.
ID C1RF_MOUSE
AC 088992;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C1q-related factor precursor.
GN C1QRF OR CRF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99097006; PubMed=9878755;
RX Berube N.G., Swanson X.H., Berttram M.J., Kittle J.D., Didenko V.,
RA Baekin D.S., Smith J.R., Pereira-Smith O.M.;
RT "Cloning and characterization of CRF, a novel C1q-related factor,
RT expressed in areas of the brain involved in motor function.";
RL Brain Res. Mol. Brain Res. 63:233-240(1999).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAINSTEM. MORE ABUNDANT IN AREAS
CC OF THE NERVOUS SYSTEM INVOLVED IN MOTOR FUNCTION, SUCH AS THE
CC PURKINJE CELLS OF THE CEREBELLUM, THE ACCESSORY OLIVARY NUCLEUS,
CC THE PONS AND THE RED NUCLEUS.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.

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CC -----
DR EMBL; AF095155; AAC64187.1; .
DR MGD; MGI:1344400; C1qrl.
DR InterPro; IPR001073; C1q.
DR InterPro; IPR000087; collagen.
DR Pfam; PF003386; C1q; 1.
DR Pfam; PF013391; Collagen; 1.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR SMART; SM00110; C1Q; 1.
DR PROSITE; PS01113; C1Q; 1.
DR Collagen; signal.
KM SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 258 C1Q-RELATED FACTOR.
FT DOMAIN 67 115 COLLAGEN-LIKE.
FT DOMAIN 123 258 C1Q.
SQ SEQUENCE 258 AA; 26485 MW; F776E2D206BFF63 CRC64;

Query Match 21.8%; Score 297.5; DB 1; Length 258;
Best Local Similarity 31.2%; Pred. No. 3; Se-18;
Matches 73; Conservative 36; Mismatches 76; Indels 49; Gaps 8;

QY 29 SPQGTGPPDCSCCHDYSFRGYGPPGPPGICPNHNGNNGATGHEGAKGKGD 88
Db 53 SEGSGAPP--STLVGPGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGK 89
QY 89 KGDLGPRERQHGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGK 134
Db 90 PGVPGPEKGEKPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPP 142
QY 135 ---IIFSSVENINIGFVMTGREGAPVGYFFTES--MKHEVEEYVYLMHNGTVE 190
Db 143 KEVLKFDVYNTLNINNDYASGKFTCNIPGYFTYHYLMNGSGGTSMWALDCKNGYRA 202
QY 191 SMYSYEMKSGKSDTSSNNAVLKAGDEYVLMNGCALH-GDHQRFSPFAGFLP 243
Db 203 SAHQADQNDVYASNSVYILHLDAGDEYFIKLDGKAKHGKSNKSYSPSGFTIY 256

RESULT 6
APM1_MOUSE STANDARD; PRT; 247 AA.
ID APM1_MOUSE 060994; 062400; 09DC68;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adiponectin precursor (30 kDa adipocyte complement-related protein)
DE (ACRP30) (Adipocyte specific protein Adipo).
GN APM1 OR ACRP30 OR ADIPOQ.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Adipocyte;
RX MEDLINE=96070757; PubMed=7592907;
RA Scherer P.E., Williams S., Fogliano M., Baldini G., Lodish H.F.;
RT "A novel serum protein similar to C1q, produced exclusively in
RT adipocytes."
RL J. Biol. Chem. 270:26746-26749(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Fibroblast;
RX MEDLINE=96209999; PubMed=8631877;
RA Hu E., Liang P., Spiegelman B.M.;

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RT "Adipo is a novel adipose-specific gene dysregulated in obesity."
RL J. Biol. Chem. 271:10697-10703(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX PubMed=11162643;
RA Das K., Lin Y., Widen E., Zhang Y., Scherer P.E.;
RT "Chromosomal localization, expression pattern, and promoter analysis
RT of the mouse gene encoding adipocyte-specific secretory protein
RT Acrp30."
RL Biochem. Biophys. Res. Commun. 280:1120-1129(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX SRAIN=C57BL/6J; TISSUE=Heart;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monnaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [5]
RP FUNCTION.
RX MEDLINE=21372498; PubMed=11479627;
RA Yamauchi T., Kamon J., Waki H., Terachi Y., Kubota N., Hara K.,
RA Mori Y., Ide T., Murakami K., Tsuboyama-Kasao N., Ezaki O.,
RA Akanuma Y., Gavrilova O., Vinson C., Reitman M.L., Kagechika H.,
RA Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., Tomita M.,
RA Froguel P., Kadowaki T.;
RT "The fat-derived hormone adiponectin reverses insulin resistance
RT associated with both lipodystrophy and obesity."
RL Nat. Med. 7:941-946(2001).
RN [6]
RP FUNCTION.
RX MEDLINE=21372499; PubMed=11479628;
RA Berg A.H., Combs T.P., Du X., Brownlee M., Scherer P.E.;
RT "The adipocyte-secreted protein Acrp30 enhances hepatic insulin
RT action."
RL Nat. Med. 7:947-953(2001).
CC -1- FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE
CC SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH
CC ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPA-B SIGNALING
CC THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED
CC EXPRESSION OF ENDOTHelial ADHESION MOLECULES. INVOLVED IN THE
CC CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.
CC -1- SUBUNIT: HOMODIGLIMER.
CC -1- SUBCELLULAR LOCATION: SECRETED IN PLASMA.
CC -1- TISSUE SPECIFICITY: SYNTHESIZED EXCLUSIVELY BY ADIPOCYTES AND
CC SECRETED INTO SERUM.
CC -1- INDUCED BY INSULIN.
CC -1- ACTIVATED BY INSULIN.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC -----
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CC -----  
 DR EMBL: U37222; AAA80543.1; -  
 DR Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 DR EMBL: U49915; AAB06706.1; -  
 DR EMBL: AF304466; AAK13417.1; -  
 DR EMBL: AK003138; BAB22597.1; -  
 DR MGD; MGI:106675; AcP30.  
 DR InterPro: IPR001073; C1q.  
 DR InterPro: IPR000087; Collagen.  
 DR Pfam: PF00386; C1q; 1.  
 DR Pfam: PF01391; Collagen; 1.  
 DR PRINTS: PRO0007; COLLENTC1Q.  
 DR SMART: SM00110; C1Q; 1.  
 DR PROSITE: PS0113; C1Q; 1.  
 DR Hormone; Collagen; Signal; Repeat; Hydroxylation; Plasma;  
 KW Polymorphism.  
 FT SIGNAL 1 17 POTENTIAL.  
 FT CHAIN 18 247 ADIPONECTIN.  
 FT DOMAIN 45 110 COLLAGEN-LIKE.  
 FT DOMAIN 111 247 C1Q.  
 FT DISULFID 39 39 INTERCHAIN (BY SIMILARITY).  
 FT MOD\_RES 47 47 HYDROXYLATION (BY SIMILARITY).  
 FT MOD\_RES 50 50 HYDROXYLATION (BY SIMILARITY).  
 FT MOD\_RES 56 56 HYDROXYLATION (BY SIMILARITY).  
 FT MOD\_RES 65 65 HYDROXYLATION (BY SIMILARITY).  
 FT MOD\_RES 79 79 HYDROXYLATION (BY SIMILARITY).  
 FT MOD\_RES 98 98 HYDROXYLATION (BY SIMILARITY).  
 FT MOD\_RES 107 107 HYDROXYLATION (BY SIMILARITY).  
 FT VARIANT 113 113 M -> V.  
 FT CONFLICT 50 50 P -> S (IN REF. 2).  
 FT CONFLICT 74 74 A -> S (IN REF. 2).  
 FT CONFLICT 117 117 A -> G (IN REF. 2).  
 FT CONFLICT 148 148 G -> N (IN REF. 2).  
 FT CONFLICT 243 243 Y -> F (IN REF. 2).  
 SQ SEQUENCE 247 AA: 26841 MM: 137B687D873988C4 CAC64:

Query Match 21.5%; Score 294; DB 1; Length 247;  
 Best Local Similarity 31.5%; Pred. No. 6.5e-18;  
 Matches 81; Conservative 40; Mismatches 102; Indels 34; Gaps 9;

QY 6 LIYVQLLFLFPLCLDDEYVESPTG--LPPDCSKCHDYSFRGYQGPFGPPG 63  
 DB 2 LLLQALLFLFLIP-SHADDVTTTELAPALVPPKGTCA-----CWMA-----GIPIG 48  
 QY 64 IPGNHNGNNGCATGHEGAKGKGDGLGPRGER---GQHGPKGKGPPIPE----- 115  
 DB 49 HPGHGTGGRDGRDGTPEKGEKGDAGLGPKEGTGVGMGTAGEPRGPGPKKGEPC 108  
 QY 116 -----LQIAFMASLATHFSNONGIIFSSVETNIGNFEDVMTGRGAPVSGVYFFFSKM 170  
 DB 109 EAAYVYRSASFVSGLETRVTPVNPVIRFTKIFYNQNMHYDGSGRKYCNIPGLYFSYHIT 168  
 QY 171 KHEDEEYVYVLMHNGTVFSYSTEKSKSPTSSNHAVALKLAKDEYVLRN-GNG---A 226  
 DB 169 VY--MKDVKVSLEFKKDKAVLFTFYDQYQEKNVDOASGVLLHLEVDQVWLQVYCGDGHNG 226  
 QY 227 LHGDHQRSTFAGFLIF 243  
 DB 227 LYADNVNDSTFTGFLLY 243

RESULT 7  
 APM1\_HUMAN STANDARD: PRT: 244 AA.  
 AC Q15848.  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Adiponectin precursor (30 kDa adipocyte complement-related protein)-  
 DE (AdRP30) (Adipose most abundant gene transcript 1) (apm-1) (Gelatin-  
 binding protein).  
 GN APM1 OR ACRP30 OR GBP28.  
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Adipose tissue;  
 RX MEDLINE=96224171; PubMed=8619847;  
 RA Maeda K., Okubo K., Shimomura I., Funahashi T., Matsuzawa Y.,  
 RA Matsubara K.;  
 RT "cDNA cloning and expression of a novel adipose specific collagen-like  
 factor, apm1 (Adipose Most abundant Gene transcript 1).";  
 RL Biochem. Biophys. Res. Commun. 221:286-289(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99196984; PubMed=10095105;  
 RA Saito K., Tobe T., Minoshima S., Asakawa S., Sumiya J., Yoda M.,  
 RA Nakano Y., Shimizu N., Tomita M.;  
 RT "Organization of the gene for gelatin-binding protein (GBP28).";  
 RL Gene 229:67-73(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99333693; PubMed=10403784;  
 RA Schaeffler A., Orso E., Palitzsch K.D., Buechler C., Drobnik W.,  
 RA Fuerst A., Scholmerich J., Schmitz G.;  
 RT "The human apm-1, an adipocyte-specific gene linked to the family of  
 TNF's and to genes expressed in activated T cells, is mapped to  
 RT chromosome 1q21.3-q23, a susceptibility locus identified for familial  
 RT combined hyperlipidemia (FCH).";  
 RL Biochem. Biophys. Res. Commun. 260:416-425(1999).  
 RN [4]  
 RP CHARACTERIZATION.  
 RX MEDLINE=20417747; PubMed=10961870;  
 RA Yokota T., Oritani K., Takahashi I., Ishikawa J., Matsuyama A.,  
 RA Ouchi N., Kihara S., Funahashi T., Tenner A.J., Iomiyama Y.,  
 RA Matsuzawa Y.;  
 RT "Adiponectin, a new member of the family of soluble defense collagens,  
 RT negatively regulates the growth of myelomonocytic progenitors and the  
 RT functions of macrophages.";  
 RL Blood 96:1723-1732(2000).  
 RN [5]  
 RP CHARACTERIZATION.  
 RX MEDLINE=20440368; PubMed=10982546;  
 RA Ouchi N., Kihara S., Arita Y., Okamoto Y., Maeda K., Kuriyama H.,  
 RA Hotta K., Nishida M., Muraguchi M., Takahashi M., Ohmoto Y.,  
 RA Nakamura T., Yamashita S., Funahashi T., Matsuzawa Y.;  
 RT "Adiponectin, an adipocyte-derived plasma protein, inhibits  
 RT endothelial NF-kappaB signaling through a C/EBP-dependent pathway.";  
 RL Circulation 102:1296-1301(2000).  
 RN [6]  
 RP FUNCTION.  
 RX MEDLINE=21372498; PubMed=11479627;  
 RA Yamauchi T., Kamon J., Waki H., Terauchi Y., Kubota N., Hara K.,  
 RA Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka N., Ezaki O.,  
 RA Akanuma Y., Gavrilova O., Vinson C., Reitman M.L., Kagechika H.,  
 RA Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., Tomita M.,  
 RA Froguel P., Kadwaki T.;  
 RT "The fat-derived hormone adiponectin reverses insulin resistance  
 RT associated with both lipodystrophy and obesity.";  
 RL Nat. Med. 7:941-946(2001).  
 RN [7]  
 RP VARIANT ADIPONECTIN DEFICIENCY CYS-112.  
 RX MEDLINE=20378830; PubMed=10918532;  
 RA Takahashi M., Arita Y., Yamagata K., Matsukawa Y., Okutomi K.,  
 RA Horie M., Shimomura I., Hotta K., Kuriyama H., Kihara S., Nakamura T.,  
 RA Yamashita S., Funahashi T., Matsuzawa Y.;  
 RT "Genomic structure and mutations in adipose-specific gene,  
 RT adiponectin.";  
 RL Int. J. Obes. Relat. Metab. Disord. 24:861-866(2000).  
 RN [8]  
 RP VARIANTS ARG-84; MET-117; THR-164; SER-221 AND PRO-241.  
 RX MEDLINE=21671103; PubMed=11812766;  
 RA Hara K., Boutin P., Mori Y., Tobe K., Dina C., Yasuda K., Yamauchi T.,  
 RA Otabe S., Okada T., Eto K., Kadwaki H., Hagiura R., Akanuma Y.,



RA Yasaki Y., Nagai R., Taniyama M., Matsubara K., Yoda M., Nakano Y.,  
 RA Kimura S., Tomita M., Kimura S., Ito C., Froguel P., Kadowaki T.,  
 RT "Genetic variation in the gene encoding adiponectin is associated with  
 an increased risk of type 2 diabetes in the Japanese population.",  
 RL Diabetes 51:536-540(2002).  
 CC -1- FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE  
 CC SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH  
 CC ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPA-B SIGNALING  
 CC THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED  
 CC EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES. INVOLVED IN THE  
 CC CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.  
 CC -1- SUBUNIT: HOMODIGLIMER (POTENTIAL).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN THE ADIPOSE TISSUE.  
 CC -1- DISEASE: Defects in APOL are the cause of adiponectin deficiency,  
 CC resulting in very low concentration of plasma adiponectin.  
 CC decreased adiponectin plasma levels are associated with obesity  
 CC Insulin resistance, and diabetes type 2.  
 CC -1- PHARMACEUTICAL: Adiponectin might be used in the treatment of  
 CC diabetes type 2 and insulin resistance.  
 CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.  
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 DR EMBL: DA5371; BAA08227.1; -  
 DR EMBL: AB012165; BAA86716.1; -  
 DR EMBL: AB012164; BAA86716.1; JOINED.  
 DR EMBL: AJ131460; CAB52413.1; -  
 DR EMBL: AJ131461; CAB52413.1; JOINED.  
 DR MIM: 605441; -  
 DR InterPro: IPR001073; C1q.  
 DR InterPro: IPR000087; Collagen.  
 DR Pfam: PF003386; C1q; 1.  
 DR Pfam: PF01391; Collagen; 1.  
 DR PRINTS: PR00007; COMPLEMENTC1Q.  
 DR SMART: SM00110; C1Q; 1.  
 DR PROSITE: PS01113; C1Q; 1.  
 DR Hormone: Collagen: Signal; Repeat; Hydroxylation; Plasma;  
 KW Polymorphism: Disease mutation; Obesity; Diabetes mellitus.  
 FT SIGNAL 1 14  
 FT CHAIN 1 244  
 FT DOMAIN 42 107  
 FT DISUFID 108 244  
 FT MOD\_RES 36 36  
 FT MOD\_RES 44 44  
 FT MOD\_RES 47 47  
 FT MOD\_RES 53 53  
 FT MOD\_RES 62 62  
 FT MOD\_RES 71 71  
 FT MOD\_RES 76 76  
 FT MOD\_RES 86 86  
 FT MOD\_RES 95 95  
 FT MOD\_RES 104 104  
 FT VARIANT 84 84  
 FT VARIANT 112 112  
 FT VARIANT 117 117  
 FT VARIANT 164 164  
 FT VARIANT 221 221  
 FT VARIANT 241 241  
 FT SEQUENCE 244 AA; 26414 MW; 64D8C6C1204B1018 CRC64;

Query Match 21.5%; Score 293.5; DB 1; Length 244;  
 Best Local Similarity 34.5%; Pred. No. 7,1e-18;  
 Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;  
 QY 53 QGP-----PGPGP-----PGIPGNHNGNNGATGAGAGKDGKDGK----LGRP---GE 97  
 DB 23 QGPVLLPLPGAGTGMAGIPGHPGNAGAPGRDGTGEKKEKEDPGLIGKSGIGE 82  
 QY 98 RGQHPGPKGKPGI-----PPE---LQIAPNASLATPESNONGIIFSSVETNIGNF 147  
 DB 83 TGVPGAGGPRGFPGLQGRKGPGEAVYRSASFVSGLETVTTPNMPRIPTKIPYNOOH 142  
 QY 148 FDVWTGPRGAPVSGVYFETSMKHEVVEYVYLMNGNTVSEMYEKKSQDTSNNH 207  
 DB 143 YDSGTGFHCNIPGLYFAHITYY--MKDVKSLEFKKRAMLETYYQYQENNVDAAGS 200  
 QY 208 AVLKAGDEYVLRM--GNG---ALHGDHREFTAGLLE 243  
 DB 201 VLHLLEVGDQVWLQVYGEGERNGILADNDSTFTGFLY 240  
 RESULT 8  
 ID COT6\_HUMAN STANDARD; PRT; 278 AA.  
 AC 09BX19;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Complement-c1q tumor necrosis factor-related protein 6 precursor.  
 GN C1QTNF6 OR CTRP6.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Piddington C.S., Sheppard P.O.;  
 RT "Homo sapiens complement-c1q tumor necrosis factor-related protein.";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RC TISSUE=Placenta;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AE329842; AKI1966.1; -  
 DR EMBL: BC020551; AAK20551.1; -  
 DR Genew: HGNC:14343; C1QTNF6;  
 DR InterPro: IPR001073; C1q.  
 DR InterPro: IPR000087; Collagen.  
 DR Pfam: PF003386; C1q; 1.  
 DR Pfam: PF01391; Collagen; 1.  
 DR PRINTS: PR00007; COMPLEMENTC1Q.  
 DR SMART: SM00110; C1Q; 1.  
 DR PROSITE: PS01113; C1Q; FALSE\_NEG.  
 KW Collagen; Signal.  
 FT SIGNAL 1 46  
 FT CHAIN 47 278  
 FT DOMAIN 97 138  
 FT DOMAIN 139 278  
 FT CARBOHYD 91 91  
 FT SEQUENCE 278 AA; 29314 MW; 64D8C6C1204B1018 CRC64;

FT CONFLICT 21 21 G -> V (IN REF. 2).  
 SQ SEQUENCE 278 AA; 30861 MM; 27A82CA863F23D47 CRC64;  
 Query Match 21.2%; Score 289.5; DB 1; Length 278;  
 Best Local Similarity 28.8%; Pred. No. 1.8e-17;  
 Matches 78; Conservative 34; Mismatches 96; Indels 63; Gaps 10.

OY 9 WOLLALFPLFCODEWESPOTGLPPDCSKC-----HGDS 48  
 DB 29 WAALLFL---MCEIRAVELTFDAVASGCCRCDCSDPLDPAIVSASSSGRHALPE 85  
 OY 49 FRGY-----QGPPEPPEPGIPGNHNGNNGATGHEGAKGKGDGLPGRGQHG 102  
 DB 86 IRPYINITLKGDKDPPGMLPGVMGREGPGGEGPGOSKGD----- 128  
 OY 103 PKGEGYGIPELQIAIAMA-----SLATFHSNNSGIIFSSVENIGNFDMRGREGA 157  
 DB 129 -KGEMGSPAP--CQKRFPAFVSGKRTALHSGEDFOTLLFERVFNLDGCDMATGQFPA 185  
 OY 158 PVSQYVFFFSMKHE-DVEEYVYVLMNGNTVFSMYSEMKGSDTSSNNAVLAKGCD 216  
 DB 186 PLRGIFYFSLVN--HSWYKETYVIMHNOKEAVILYA-QPSERSIMQSQVMDLAYGD 242  
 OY 217 EVMLRM-----GNGALHGDHOFSTFAGFL 242  
 DB 243 RYVWRLFKRENALYSNDPFIYFSGHLI 273

RESULT 9  
 GLIC\_MOUSE STANDARD; PRT; 255 AA.  
 AC Q9ESN4;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 15-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Gliacolin precursor.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20428709; PubMed=10862616;  
 RA Koide T., Aso A., Yorifuji T., Nagata K.;  
 RT "Conformational requirements of collagenous peptides for recognition  
 by the chaperone protein HSP47.";  
 RL J. Biol. Chem. 275:27957-27963(2000).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN GLIAL CELLS.  
 CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 C10 DOMAIN.  
 CC -----  
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 CC -----  
 CC DR EMBL; AB044560; BAB15806.1; -  
 CC DR InterPro; IPR001073; C1g.  
 CC DR InterPro; IPR000087; Collagen.  
 CC DR Pfam; PF00386; C1g; 1.  
 CC DR Pfam; PF01391; Collagen; 1.  
 CC DR PRINTS; PRO0007; COMPLENCT10.  
 CC DR SMART; SMO0110; C10; 1.  
 CC DR PROSITE; PS01113; C10; 1.  
 CC KW Collagen; Signal.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 255 GLIACOLIN.  
 FT DOMAIN 61 111 COLLAGEN-LIKE.  
 FT DOMAIN 120 255 C10.  
 SQ SEQUENCE 255 AA; 26687 MM; 529FBAF4B2191BC1 CRC64;

Query Match 20.9%; Score 285.5; DB 1; Length 255;  
 Best Local Similarity 34.2%; Pred. No. 3.5e-17;  
 Matches 68; Conservative 32; Mismatches 82; Indels 17; Gaps 5;

OY 61 PPGIPGNHNGNNGATGHEGAKGKGDGLPGRGQHGPKGEGKYPGIPPELQIAF 120  
 DB 56 PPFIGPKKEAPGRPKACPRGPGPPGVPQPPGKEKEPGKGLPBPQ--APGILNAG 114  
 OY 121 MASLATH-----FSNONGS---ITFSSVENIGNFDMRGREGAVSGYFEFT 166  
 DB 115 AISAATYSTVPKIAEYAGIKRQHEGYELKFDVYVNLNHNHDPPTGKTCSTPGIYFT 174  
 OY 167 FS-IMKHEDVEEYVYVLMNGNTVFSMYSEMKGSDTSSNNAVLAKGDEYVLMNGNG 225  
 DB 175 YHVLMRGDGTSMADLCNNQVRSALINQDADQNDVANSVYLHLBERGDEYVYRLDGG 234  
 OY 226 ALH-GDHOESTFAGFLF 243  
 DB 235 KAHGNNNNKYSTFSGFIY 253

RESULT 10  
 CALA\_CHICK STANDARD; PRT; 674 AA.  
 AC P08125;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Collagen alpha 1(X) chain precursor.  
 GN COL10A1.  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 CC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE OF 48-674 FROM N.A., AND SEQUENCE OF 103-117 AND 453-466.  
 RX MEDLINE=86168227; PubMed=3082876;  
 RA Luvalle P., Ninomiya Y., Rosenblum N.D., Olsen B.R.;  
 RA Ninomiya Y., Gordon M., van der Rest M., Schmid T., Linsenmayer T.,  
 RA Olsen B.R.;  
 RT "The developmentally regulated type X collagen gene contains a long  
 open reading frame without introns.";  
 RL J. Biol. Chem. 261:5041-5050(1986).  
 RN [2]  
 RP SEQUENCE OF 1-75 FROM N.A.  
 RX MEDLINE=89054019; PubMed=2461368;  
 RA Luvalle P., Ninomiya Y., Rosenblum N.D., Olsen B.R.;  
 RT "The type X collagen gene. Intron sequences split the 5'-untranslated  
 region and separate the coding regions for the non-collagenous amino-  
 terminal and triple-helical domains.";  
 RL J. Biol. Chem. 263:18378-18385(1988).  
 RN [3]  
 RP REVISIONS TO C-TERMINUS.  
 RX MEDLINE=89380199; PubMed=2476437;  
 RA Yamaguchi N., Benay P.D., van der Rest M., Ninomiya Y.;  
 RT "The cloning and sequencing of alpha 1(VIII) collagen cDNAs  
 demonstrate that type VIII collagen is a short chain collagen and  
 contains triple-helical and carboxyl-terminal non-triple-helical  
 RT domains similar to those of type X collagen.";  
 RL J. Biol. Chem. 264:16022-16029(1989).  
 CC -1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTROPHIC  
 CC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE  
 CC MINERALIZATION ZONES OF HYALINE CARTILAGE.  
 CC -1- SUBUNIT: HOMOTRIMER.  
 CC -1- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING  
 CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.  
 CC -1- SIMILARITY: STRONG. TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.  
 CC -1- SIMILARITY: CONTAINS 1 C10 DOMAIN.  
 CC -----  
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|                       |                 |                   |           |            |
|-----------------------|-----------------|-------------------|-----------|------------|
| Query Match           | 20.5%           | Score 280.5       | DB 1      | Length 674 |
| Best Local Similarity | 30.9%           | Pred. No. 2.7e-16 |           |            |
| Matches 76            | Conservative 23 | Mismatches 90     | Indels 57 | Gaps 5     |

|            |  |           |      |         |
|------------|--|-----------|------|---------|
| RESULT 11  |  |           |      |         |
| CA1A_MOUSE |  |           |      |         |
| ID         | CA1A_MOUSE   | STANDARD: | PRT: | 680 AA. |
| AC         | Q05306;  |           |      |         |
| DT         | 01-NOV-1995 (Rel. 32, Created)   |           |      |         |
| DT         | 01-NOV-1995 (Rel. 32, Last sequence update)                            |           |      |         |
| DT         | 01-NOV-1995 (Rel. 32, Last annotation update)                          |           |      |         |
| DE         | Collagen alpha 1(X) chain precursor.                                   |           |      |         |
| GN         | COL10A1.   |           |      |         |
| OS         | Mus musculus (Mouse).  |           |      |         |
| OC         | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |           |      |         |
| OC         | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.              |           |      |         |
| OX         | NCBI_TaxID=10090;  |           |      |         |
| RN         | [1]  |           |      |         |
| RP         | SEQUENCE FROM N.A.   |           |      |         |
| RC         | STRAIN-BALB/c.   |           |      |         |
| RX         | MEDLINE=93143676; PubMed=8424763;                                      |           |      |         |
| RA         | Elima K., Berola I., Rosati R., Metsaranta M., Garofalo S., Perala M., |           |      |         |
| RA         | de Crombrugne B., Vuorio E.;   |           |      |         |
| RT         | "The mouse collagen X gene: complete nucleotide sequence, exon         |           |      |         |
|            | structure and expression pattern.";                                    |           |      |         |

```

RL Biochem J. 289:247-253(1993).
EN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV; TISSUE=Liver;
RX MEDLINE=93238750; PubMed=8477738;
RA Kong R.Y.C., Kwan K.M., Lau E.T., Thomas J.T., Boot-Handford R.P.,
RA Grant M.E., Cheah K.S.E.;
RT "Intron-exon structure, alternative use of promoter and expression of
RT the mouse collagen x gene, Col10a-1.";
RL Eur. J. Biochem. 213:99-111(1993).
RN [3]
RP SEQUENCE OF 51-680 FROM N.A.
RC STRAIN=DBA/2J;
RX MEDLINE=92267014; PubMed=1587271;
RA Ape S.S., Seldin M.F., Hayashi M., Olsen B.R.;
RT "Cloning of the human and mouse type X collagen genes and mapping of
RT the mouse type X collagen gene to chromosome 10.";
RL Eur. J. Biochem. 206:217-224(1992).
RN [4]
RP SEQUENCE OF 385-627 FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=92182017; PubMed=1543751;
RA Elima K., Meseaeranta M., Kallio J., Perazael M., Eerola I.,
RA Garofalo S., de Crombrughe B., Vuorio E.;
RT "Specific hybridization probes for mouse alpha 2(Ix) and alpha 1(X)
RT collagen mRNAs.";
RL Biochim. Biophys. Acta 1130:78-80(1992).
CC -1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTROPHIC
CC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUPRATIVE
CC MINERALIZATION ZONES OF HYALINE CARTILAGE.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- PFM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC -1- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC -----
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CC -----
CC
DR EMBL, X67348; CAA47763.1; -
DR EMBL, X65121; CAA46237.1; -
DR EMBL, X63013; CAA44741.1; -
DR EMBL, Z21610; CAA79736.1; -
DR PIR, S28807; S28807.
DR PIR, S31216; S31216.
DR PIR, S22215; S22215.
DR MGD; MGI:88445; Col10a1.
DR InterPro: IPR001073; C1q.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; C1q; 1.
DR Pfam: PF01391; Collagen; 9.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR Prodom: PD000007; Collagen; 2.
DR SMART; SM00110; C1Q; 1.
DR PROSITE; PS01113; C1Q; 1.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Cartilage; Collagen; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 680 COLLAGEN ALPHA 1(X) CHAIN.
FT DOMAIN 19 56 NONHELICAL REGION (NC2).
FT DOMAIN 57 519 TRIPLE-HELICAL REGION.
FT DOMAIN 520 680 NONHELICAL REGION (NC1).
FT DOMAIN 545 680 C1Q.
FT CONFLICT 248 248 P -> L (IN REF. 3).
FT CONFLICT 286 286 A -> S (IN REF. 2).
FT CONFLICT 306 305 L -> F (IN REF. 3).
FT CONFLICT 417 417 T -> S (IN REF. 3).
FT CONFLICT 451 451 R -> K (IN REF. 4).

```

FT CONFLICT 500 500 H -> L (IN REF. 3).  
 FT CONFLICT 567 567 A -> C (IN REF. 3).  
 FT CONFLICT 569 569 I -> H (IN REF. 3).  
 FT CONFLICT 571 572 FD -> IX (IN REF. 3).  
 FT CONFLICT 635 635 O -> T (IN REF. 3).  
 SO SEQUENCE 680 AA: 66775 MM: FE984CA99AF708E2 CRC64:

Query Match 20.4%; Score 278.5; DB 1; Length 680;  
 Best Local Similarity 30.5%; Pred. No. 4.1e-16;  
 Matches 73; Conservative 34; Mismatches 87; Indels 45; Gaps 7;

Y 45 GDYSTRGQGPFGPPGPGPGICPGNHNNGNNGATG-----HEGAKGKDGKGLGPRGEG 99  
 D 443 GEPGIPGTRGPPGPGVPCPGSKGDPGNPAGAPAGIATKGLNPTGPPGPGRGHSG 502  
 Y 100 QHGPKEGKGPICP-----PELQIA-----FMASLATHF 128  
 D 503 EPGLPGRPPGPPGPGQAVMPDGFITAGQRPRLSGMPVLSANIGVGMPSATVILSKRX 562  
 Y 129 SNQSGIIFSSVETNIGNPFDMVTRFGAPVSGVYFFTFSMKHEDVEEYVYLHNGNT 188  
 D 563 PAYGAPIDPFDELLYNRQOHYDPRSGITFKIPGIYFYSYHV--HWKGTWVGLYKNGTP 620  
 Y 189 VFSWSTYE--MKGSDTSSNNAVYLKLAGDEVWLMGN---GALGDRHORETFAGFL 242  
 D 621 --TMTYDEYSKGYLDQASGSAIMELTENDQVWLQLPNAGSNGLYSSEYVHSSFGFLV 677

RESULT 12  
 CA1A\_BOVIN STANDARD: PRT: 674 AA.  
 AC P23206;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Collagen alpha 1(X) chain precursor.  
 GN COL10A1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cartilage;  
 RX MEDLINE=9113131; PubMed=1703407;  
 RA Thomas J.T., Kwan A.P.L., Grant M.E., Boot-Handford R.P.;  
 RT "Isolation of cDNAs encoding the complete sequence of bovine type X  
 collagen. Evidence for the condensed nature of mammalian type X  
 collagen genes.";  
 RT Biochem. J. 273:141-148(1991).  
 CC -1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC  
 CC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE  
 CC MINERALIZATION ZONES OF HALINE CARTILAGE.  
 CC -1- SUBUNIT: HOMOTRIMER.  
 CC -1- PPM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING  
 CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.  
 CC -1- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.  
 CC -1- SIMILARITY: CONTAINS 1 C10 DOMAIN.  
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 CC EMBL: X53556; CAA37624.1; -  
 CC PIR: S13301; S13301.  
 CC InterPro: IPR001073; C1g.  
 CC InterPro: IPR000087; Collagen.  
 CC Pfam: PF00386; C1g; 1.

DR Pfam: PF01391; Collagen. 9.  
 DR PRINTS: PR00007; COMPLEMENTC1Q.  
 DR ProDom: PD000007; Collagen. 1.  
 DR SMART: SM00110; C1Q; 1.  
 DR PROSITE: PS01113; C1Q; 1.  
 KW Extracellular matrix; connective tissue; Repeat; Hydroxylation;  
 KW Cartilage; Collagen; Signal; Glycoprotein.  
 FT SIGNAL 1 18  
 FT CHAIN 19 674 COLLAGEN ALPHA 1(X) CHAIN.  
 FT DOMAIN 19 56 NONHELICAL REGION (NC2).  
 FT DOMAIN 57 519 TRIPLE-HELICAL REGION.  
 FT DOMAIN 520 674 NONHELICAL REGION (NC1).  
 FT DOMAIN 539 674 C1Q.  
 FT DISULFID 194 197 BY SIMILARITY.  
 FT MOD\_RES 460 460 HYDROXYLATION (BY SIMILARITY).  
 FT MOD\_RES 463 463 HYDROXYLATION (BY SIMILARITY).  
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. (POTENTIAL)).  
 SO SEQUENCE 674 AA: 65546 MM: CDACAT3A03E004CA CRC64:

Query Match 20.1%; Score 275; DB 1; Length 674;  
 Best Local Similarity 30.0%; Pred. No. 8e-16;  
 Matches 72; Conservative 31; Mismatches 87; Indels 50; Gaps 6;

Y 51 GYQGPFGPPGPPGPGPGICPGNHNNGNNGATGHEGAKGKGD-----KDLGPRGEG 99  
 D 434 GNGEAGRGPGVGPICPTGRPIGPPGPGSKGDPVTPGPPGAGIAYKVGNGPTGPG 493  
 Y 100 QHGPKEGKGPICP-----PELQIA-----FMASLATHFSNNGSI----- 136  
 D 494 PPGPGNMGEPGLPPGPPGPGPGQVALPEDFVKAGQRPVSAVANGVGMPSATVILS 553  
 Y 137 -----FSSVETNIGNPFDMVTRFGAPVSGVYFFTFSMKHEDVEEYVYLHNG 185  
 D 554 KAYPAIGTPIRPDKILYKNQOHYDPTGTGTFCKIPGIYFYSYHI--HWKGTWVGLYK 611  
 Y 186 GNTVSMSTYEKKGSDTSSNNAVYLKLAGDEVWLMN---GNGALGDRHORETFAGFL 242  
 D 612 GTPVMTYTYDEYIKGYLDQASGSAVIDLTENDQVWLQLPNAGSNGLYSPEYVHSSFGFLV 671

RESULT 13  
 C1QC\_MOUSE STANDARD: PRT: 246 AA.  
 ID C1QC\_MOUSE  
 AC 002105;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Complement C1q subcomponent, C chain precursor.  
 GN C1Q OR C1QC.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ICR; TISSUE=Macrophage;  
 RX MEDLINE=9301118; PubMed=1396691;  
 RA Petry F., Reid K.B.M., Loos M.;  
 RT "Isolation, sequence analysis and characterization of cDNA clones  
 RT coding for the C chain of mouse C1q. Sequence similarity of  
 RT complement subcomponent C1q, collagen type VIII and type X and  
 RT precerebellin.";  
 RT Eur. J. Biochem. 209:129-134(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Liver;  
 RX MEDLINE=96186528; PubMed=8606057;  
 RA Petry F., McClive P.J., Botto M., Morley B.J., Morahan G., Loos M.;  
 RT "The mouse C1q gene are clustered on chromosome 4 and show  
 RT conservation of gene organization.";  
 RT Immunogenetics 43:370-376(1996).  
 CC -1- FUNCTION: C1Q ASSOCIATES WITH THE PROENZYMES C1R AND C1S TO YIELD  
 CC C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE





Db 537 TPVLSANGVTGMPVSAFTVLSKAYPAIGTPIPEDKILYNRQGHYDPRGTGFTQIPGI 596  
 QY 163 YFFPFSMAKHEDVEEYVYLHANGNTVFSWYSEKKGSDPTSSNNAVLKAKGDEVWLRM 222  
 Db 597 YFFSYHV--HVKGTHVWGLTKRNGTPVMTYDEYTKGYLDQASGSAITLTDNDVWLQL 654  
 QY 223 GN---GALHGDHQRSTPAGFL 242  
 Db 655 PNAESNGLYSESYVHSSPSGFLV 677

## RESULT 15

COT5\_HUMAN STANDARD; PRT; 243 AA.  
 ID COT5\_HUMAN STANDARD; PRT; 243 AA.  
 AC Q9BXJ0; Q9UEY4;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Complement-clq tumor necrosis factor-related protein 5 precursor.  
 GN C1QTNF5 OR CTRP5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sheppard P.O., Humes J.M.;  
 RT "Homo sapiens complement-clq tumor necrosis factor-related protein.";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 25-243 FROM N.A.  
 RC TISSUE=uterus;  
 RA Ottenwaelder B., Obermaier B., Mewes H.-W., Gassenhuber J.,  
 RA Wiemann S.;  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC DR EMBL; AF329841; AKI17965.1; -  
 CC DR EMBL; AL110261; CAB53702.1; -  
 CC DR Genew; HGNC:14344; C1QTNF5.  
 CC DR InterPro; IPR001073; C1Q.  
 CC DR InterPro; IPR000087; Collagen.  
 CC DR Pfam; PF00386; C1q; 1.  
 CC DR Pfam; PF01391; Collagen; 1.  
 CC DR PRINTS; PR00007; COMPLEMENTC1Q.  
 CC DR SMART; SM00110; C1Q; 1.  
 CC DR PROSITE; PS01113; C1Q; FALSE\_NEG.  
 CC KM Collagen; Signal.  
 CC FT SIGNAL 1 15 POTENTIAL.  
 CC FT CHAIN 16 243 COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-  
 CC FT DOMAIN 30 95 RELATED PROTEIN 5.  
 CC FT DOMAIN 97 243 COLLAGEN-LIKE.  
 CC SQ SEQUENCE 243 AA; 25298 MW; 7CCDA65CDA7EB784 CRC64;  
 Query Match 19.3%; Score 264.5; DB 1; Length 243;  
 Best Local Similarity 32.6%; Pred: No. 2e-15;  
 Matches 74; Conservative 35; Mismatches 93; Indels 25; Gaps 9;  
 QY 34 GLPP-DCSK---CHGDYSEFRTYGGPPGPGPGIPIGNHNGNNGATGHEGAKGE----- 85  
 Db 15 GSPPLDNKIPSLCPG---HPGLPTPGHNSOGLPGRDGRDGRDGAAGAGEGEGGRP 71  
 QY 86 --KGDKGDLGRGRGQHGRGKGRGPGIPELQIAFMASLATHFNSQNSGIIFSSVETN 143

Db 72 GLPGRGDPGPRGEGAPGAPPTGPAGECSYPPRSASFSAKRSESRVPPSDAPLPEDRVLYN 131  
 QY 144 IGFEDVMTGRGAPVSGVYFFTSMKHEDVEEYVY--LHANGNTVFSWYSEKKG-- 199  
 Db 132 ECGHYDAVATGKFTQCPGVYFAY---HATVYRASLQFDLYKNESIASFFQF-FGQMP 186  
 QY 200 KSDTSSNNAVLKAKGDEVWLMGNG---ALHGDHQRSTPAGFLF 243  
 Db 187 KPAISLGGAMVRLPEPDQVWVQGVGDYIGIYASIKTDTSTESGFLVY 233

Search completed: January 15, 2003, 19:38:01  
 Job time : 40 secs





```
QY 61 PGPIGNHNGNNGATGHEGAKGKGDGLGPRGEGOHGPKGKGYPIPELOIAF 120
DB 61 PPGIENHNNNGATGHEGAKGKGDGLGPRGEGOHGPKGKGYPIPELOIAF 120
QY 121 MASLATHFNSQNGIIFSSVETNIGNFPDVMTRGFGAPVSGYFFFTFSMKHEDVEEYV 180
DB 121 MASLATHFNSQNGIIFSSVETNIGNFPDVMTRGFGAPVSGYFFFTFSMKHEDVEEYV 180
QY 181 YLMHNGNTVFSYSTEEMKKSQSSNHAVALKLAKDEWVLRMGNGALHGHORESTFAG 240
DB 181 YLMHNGNTVFSYSTEEMKKSQSSNHAVALKLAKDEWVLRMGNGALHGHORESTFAG 240
QY 241 LLEFETK 246
DB 241 LLEFETK 246

RESULT 2
QY 09D8U4 PRELIMINARY: PRT: 294 AA.
AC 09D8U4
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 1810033K05RIK protein.
CN 1810033K05RIK
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Araiwa T., Hara A., Fukunishi Y., Kono H., Aachi Y., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., But C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK007683; BAB25187.1; -
DR MGI: 1916433; 1810033K05RIK.
DR InterPro: IPR001073; Clq.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; Clq; 1.
DR Pfam: PF01391; Collagen; 2.
DR PRINTS: PR00007; COMPLEMENTC1Q.
DR SMART: SM00110; C1Q; 1.
DR PROSITE: PS01113; C1Q; 1.
SQ SEQUENCE 294 AA; 30865 MW; 6D3905AE7C19B6FA CRC64;

Query Match 22.9%; Score 313; DB 11; Length 294;
Best Local Similarity 28.9%; Pred. No. 3.8e-20;
Matches 86; Conservative 41; Mismatches 89; Indels 82; Gaps 12;
```

```
QY 60 GPPGIPGNHNGNNGATGHEGAKGKGD-----L 92
DB 55 GPPGAPGSSGVYVGRGPFCKDGDGDGSGEGEPGPRGNKCKPKKACAGCA 114
QY 93 GPRGER-----GQHPKGEKGYPIPE-----PELOIAFMASLATHFNSQNS 133
DB 115 GPRGKGVSGTCKHGTGCKKPKKKGEPGLPGCSCSSRAKSAFSAVAKSYRELU 174
QY 134 GIFFSSVETNIGNFPDVMTRGFGAPVSGYFFFTFSMKHEDVEEYVYLMHNGNTVF 190
DB 175 PIKFKIILNNEGHNASGKFEVCSVPGIYFTYDITLANK-----LAIGLVHNGO--Y 227
QY 191 SMYSYEMK-GKSDTSSNHAVALKLAKDEWVLRM-----GNGLAHGHORESTFAGLE 243
DB 228 RIRTFDANTGNHDVASGSTLTALKEGDEWVLOIFYSEONGLFYDPYWDLSFTGFLY 285

RESULT 3
QY 095M04 PRELIMINARY: PRT: 240 AA.
AC 095M04
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adipose tissue-specific protein adipo Q.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21369933; PubMed=11382781;
RA Sato C., Yasukawa Z., Honda N., Matsuda T., Kitajima K.;
RT "Identification and Adipocyte Differentiation-dependent Expression of
RT the Unique Disialic Acid Residue in an Adipose Tissue-specific
RT Glycoprotein, Adipo Q."
RL J. Biol. Chem. 276:28849-28856(2001).
DR EMBL: AF269230; AAK58902.1; -
DR InterPro: IPR001073; Clq.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; Clq; 1.
DR Pfam: PF01391; Collagen; 1.
DR ProDom: PD000007; Collagen; 1.
DR PROSITE: PS01113; C1Q; UNKNOWN; 1.
SQ SEQUENCE 240 AA; 26091 MW; C6253BA803B9A668 CRC64;

Query Match 21.9%; Score 289; DB 6; Length 240;
Best Local Similarity 33.3%; Pred. No. 5.4e-19;
Matches 75; Conservative 35; Mismatches 85; Indels 30; Gaps 7;

QY 44 HGDYSEFRGYGPPGPPG-----PGIPGNHNGNNGATGHEGAKGKGDGD---LGR 95
DB 16 HGEDNM---EDPRLPKGACAGMAGIPGPHNGTPGRGRGRTGCEKEKGDAGLGRK 72
QY 96 GER-----GQHPKGEKGYPIPE-----LQIAFMASLATHFNSQNGIIFSSVET 142
DB 73 GETGDVGMTCGAGPRGPFPTPKRKEPGEAAYVYSASFVSGLETRVYVNVDIRFKIFY 132
QY 143 NIGNFPDVMTRGFGAPVSGYFFFTFSMKHEDVEEYVYLMHNGNTVFSYSEMKGSD 202
DB 133 NOONHTDGSCTGKFCYCNIPGLYFSTHITVY--MKDVKSFLFKKRAVLFYTDYOKEKND 190
QY 203 TSSNHAVALKLAKDEWVLRMGNGALH-----GDHORESTFAGLE 243
DB 191 QASGSVLLHLEVGDDVWLVQVYEGENHNGVYADNVNDSTFTGFLY 235

RESULT 4
QY 095J07 PRELIMINARY: PRT: 243 AA.
AC 095J07
```



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Db      1074   EXQ_1076

RESULT 7
ID       Q9Z1K4          PRELIMINARY;             PRT;           295 AA.
AC       Q9Z1K4:
DT       01-MAY-1999 (TREMBLrel. 10, Created)
DT       01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT       01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE       Collagen alpha 1 type X (Fragment).
GN       COL10A1.
OS       Rattus norvegicus (Rat).
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN       NCBI_TaxID=10116;
RP       (1)
RR       SEQUENCE FROM N.A.
RC       STRAIN=SPRAGUE-DAWLEY;
RX       MEDLINE=20310874; PubMed=10853827;
RA       Marks S.A., Lundmark C., Christersson C., Wurtz T., Odgren P.R.,
RA       Selfert M.F., Mackay C.A., Mason-Savva A., Popoff S.E.;
RT       Endochondral bone formation in toothless (osteopetrotic) rats:
RT       failures of chondrocyte patterning and type x collagen expression.";
RL       Int. J. Dev. Biol. 44:309-316(2000).
DR       EMBL, AJ131848; CAA10518.1; -.
DR       InterPro; IPR001073; Clq.
DR       InterPro; IPR000087; Collagen.
DR       Pfam; PF00386; Clq; 1.
DR       Pfam; PF01391; collagen; 3.
DR       PRINTS; PR00007; COMPLEMENTC1Q.
DR       SMART; SM01110; Clq; 1.
DR       PROSITE; PS01113; Clq; 1.
FT       NON_TER
SQ       SEQUENCE      295 AA; 30012 MW; FF43B1548028813E CRC64;

Query Match              19.8%; Score 270; DB 11; Length 295;
Best Local Similarity    30.2%; Pred. No. 2.8e-16;
Matches 73; Conservative 34; Mismatches 87; Indels 48; Gaps

QY      45 GDYSRGYGCGPGPGPCGIPGNGHNCNNGCATG-----HEGAKEGCKDGLGPR--G 96
        : : : : | | | | | | | | : : : : : : : : : : : : : : | | | |
DB      55 GEPIGTGRGPIRGPIRGICGFPSKSDPKPCAFAGIYTKLNKPAGPGRGPRGHG 114
        : : : : | | | | | | | | : : : : : : : : : : : : : : | | | |

QY      97 ERGOHGPKGEKGYPGIPPELDI-----ATMASIA 125
        : : : : | | | | : : : : : : : : : : : : : : : : : : : :
DB      115 EPGLPGPGPGPPGPPOAVIPDGFTKSGQRPLSGMPLVSANGVGMPSAFIVILS 174
        : : : : | | | | : : : : : : : : : : : : : : : : : : : :

QY      126 TRFSNQNGCIIFSSVETINIGNEFDVMTGRCAPGVGYFFTSMMKHEDVEEVYYLMHN 185
        : : : : | | | | : : : : : : : : : : : : : : : : : : : :
DB      175 KAYPAVGAPIPFDELIVNRQOHYDPRSGIFTCKIGIYFESYHI--HWKGTWVMWGIVKN 232
        : : : : | | | | : : : : : : : : : : : : : : : : : : : :

QY      186 GNTVPMASYE--MKGSKDTSSNAHVLLAKGDENVLRNGN---CALGHDHREFSTFAGE 240
        : : : : | | : : | : : : : : : : : : : : : : : : : : : :
DB      233 GTP--TMITYDEYKSGYLDAQSAIMEITENDQVWLDPNANESNGLYSSEYVHSFSGF 290
        : : : : | | : : | : : : : : : : : : : : : : : : : : : :

QY      241 LV 242
        : :
DB      291 LV 292

RESULT 8
ID       Q9H667          PRELIMINARY;             PRT;           158 AA.
AC       Q9H667:
DT       01-MAR-2001 (TREMBLrel. 16, Created)
DT       01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT       01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE       CDNA: FLJ22569 fis, clone HSI02142 (Hypothetical 17.6 kDa
DE       protein).
OS       Homo sapiens (Human).
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX       Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SMALL INTESTINE;
RA Matsumae K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA Suzuki Y., Ohbayashi M., Nishi T., Shibahara T., Tanaka T.,
RA Nakamura Y., Isgai T., Sugano S.;
RT "NEO human cDNA sequencing project."
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Strausberg R.;
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK026222; BAB15396.1; -
DR EMBL: BC007520; AAH07520.1; -
DR InterPro: IPR01073; Clq.
DR Pfam: PF00386; Clq. 1.
DR PRINTS: PR00007; COMPLEMENTC1Q.
DR SMART: SM00110; Clq. 1.
DR PROSITE: PS01113; Clq; UNKNOWN_1.
DR Hypothetical protein.
SQ SEQUENCE 158 AA; 17625 MW; 47DB10EDD6DC9760 CRC64;

Query Match 19.5%; Score 266.5; DB 4; Length 158;
Best Local Similarity 37.0%; Pred. No. 2.7e-16;
Matches 51; Conservative 36; Mismatches 48; Indels 3; Gaps 2

QY 109 YGIPPELOIAFMASLAFHS--NONGTIFSSVENTIGNFPMVTGREGAPVSGVYFET 166
DB 21 YF-LQOMNVAASARTSLAPGTLDPYVFLNLNIGETDLDLGRNCVNGTYFI 79
QY 167 FSMKHEDEVYVYLMHNGNTVFMSYEMKGSKDSSTSSNAAVLAKDEYVLRMGCA 226
DB 80 FHLKLAIVAVPLVYMLMKNEEVLVSAYANDGAPDHETASNHAILDLQFGDDQITLRLHGA 139
QY 227 LMGDHORSTFAGFLFE 244
DB 140 IYGSMSKYSTFGSYLDLYQ 157

RESULT 9
Q8TEJ5 PRELIMINARY; PRT; 705 AA.
AC Q8TEJ5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE FLJ00201 protein (Fragment).
GN FLJ00201.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
RT "The nucleotide sequence of a long cDNA clone isolated from human
RL spleen."
RL Submitted (Jan-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK074129; BAB84955.1; -.
FT NON TER 1
SQ SEQUENCE 705 AA; 67430 MW; 07DB85A65A948ED3 CRC64;

Query Match 18.9%; Score 258.5; DB 4; Length 705;
Best Local Similarity 31.6%; Pred. No. 8.4e-15;
Matches 79; Conservative 24; Mismatches 92; Indels 55; Gaps 8;

QY 45 GDYSRGRGQPPGPGPGICIRGNHGNNGNNGATGHEGAKGEGKDGDLGPRGE-----R 98
DB 462 GPSGIGAGGAGPGAGPGGGLDLKKEPGLPGPG-EGRAGEGRTAGPGPGVPGSPGIT 520

```



RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Cuslinsich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K., -F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whittaker C., Wilmberg L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 DR EMBL: AK018742; BAB31383.1; -  
 DR MGD: MGI:88463; Col8a1.  
 DR InterPro: IPR001073; C1q.  
 DR InterPro: IPR000087; Collagen.  
 DR Pfam: PF00386; C1q; 1.  
 DR Pfam: PF01391; Collagen; 7.  
 DR PRINTS: PR00007; COMPLEMENTC1Q.  
 DR SMART: SM00110; C1Q; 1.  
 DR PROSITE: PS01113; C1Q; 1.  
 SQ SEQUENCE 744 AA; 73581 MW; C659BDCBCD6EB9C CRC64;

Query Match 18.8%; Score 257; DB 11; Length 744;  
 Best Local Similarity 29.6%; Pred. No. 1,2e-14;  
 Matches 77; Conservative 27; Mismatches 102; Indels 54; Gaps 6;

OY 34 GLPPDCSCCHGDSFSGYOGPPPPGPIPGHNGNNGATGCHGA-----KGE 85  
 DB 487 GIPGD--QGLOGPPGIGVPGSPGIPGIPGKGGPGLPGPPGPGVGRVAGLHGP 544  
 OY 86 KGDGDLGPPRGEGOHGPKGKGYPCIP-----PELQI-----118  
 DB 545 PGKRGALGPGQGPPLPPPPGPPGPPAVMPPTSPGEGYLPDGLGIDGVKPPHAYAGK 604  
 OY 119 -----AFMASLATHFSNONGIIFSSVETNIGNEFDVWTRFGAPVSGVFEFT 166  
 DB 605 KKGHGPAVEPAFTALFTVPPVGAPEKDKLLYNQRQYNTQGTGIFCEVPGVYFA 664  
 OY 167 FSNMKHEDVEEYVYLLMHNGTIVSMYSYEKKGSDTSSNNAVLKLAGDEVLMRGN-- 224  
 DB 665 YHV--HCKGGMVVALFKNNPMMYTYDEYKKGFLDQASGSAVILLRPGDQVFLQMPSEQ 722  
 OY 225 -GALHGDHORESTFAGFLF 243  
 DB 723 AAGLYAGQVHSSFSGYLLY 742

## RESULT 13

0921S8 PRELIMINARY; PRT; 744 AA.

AC 0921S8;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Procollagen, type VIII, alpha 1.  
 GN COL8A1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.,  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC011061; AAH1061.1; -  
 DR MGD: MGI:88463; Col8a1.  
 DR InterPro: IPR001073; C1q.  
 DR InterPro: IPR000087; Collagen.  
 DR Pfam: PF00386; C1q; 1.  
 DR Pfam: PF01391; Collagen; 7.  
 DR PROSITE: PS01113; C1Q; UNKNOWN\_1.  
 KW Collagen.  
 SQ SEQUENCE 744 AA; 73621 MW; BF7A7ED79D8463AA CRC64;

Query Match 18.8%; Score 257; DB 11; Length 744;  
 Best Local Similarity 29.6%; Pred. No. 1,2e-14;  
 Matches 77; Conservative 27; Mismatches 102; Indels 54; Gaps 6;

OY 34 GLPPDCSCCHGDSFSGYOGPPPPGPIPGHNGNNGATGCHGA-----KGE 85  
 DB 487 GIPGD--QGLOGPPGIGVPGSPGIPGIPGKGGPGLPGPPGPGVGRVAGLHGP 544  
 OY 86 KGDGDLGPPRGEGOHGPKGKGYPCIP-----PELQI-----118  
 DB 545 PGKRGALGPGQGPPLPPPPGPPGPPAVMPPTSPGEGYLPDGLGIDGVKPPHAYAGK 604  
 OY 119 -----AFMASLATHFSNONGIIFSSVETNIGNEFDVWTRFGAPVSGVFEFT 166  
 DB 605 KKGHGPAVEPAFTALFTVPPVGAPEKDKLLYNQRQYNTQGTGIFCEVPGVYFA 664  
 OY 167 FSNMKHEDVEEYVYLLMHNGTIVSMYSYEKKGSDTSSNNAVLKLAGDEVLMRGN-- 224  
 DB 665 YHV--HCKGGMVVALFKNNPMMYTYDEYKKGFLDQASGSAVILLRPGDQVFLQMPSEQ 722  
 OY 225 -GALHGDHORESTFAGFLF 243  
 DB 723 AAGLYAGQVHSSFSGYLLY 742

## RESULT 14

095395 PRELIMINARY; PRT; 194 AA.

AC 095395;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Adiponectin (Fragment).  
 GN ADEL.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=ADIPOSE TISSUE;  
 RA Kabir M., Anantharayan S., Ionut V., Kim S.P., Van Citters G.W.,  
 RA Des M.K., Bergman R.N.;  
 RT "Regulation of Adiponectin gene expression in the fat-fed dog."  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF417206; AAL09702.1; -  
 DR InterPro: IPR001073; C1q.  
 DR InterPro: IPR000087; Collagen.  
 DR Pfam: PF00386; C1q; 1.  
 DR Pfam: PF01391; Collagen; 1.  
 DR ProDom: PD000007; Collagen; 1.  
 DR PROSITE: PS01113; C1Q; UNKNOWN\_1.  
 FT NON\_TER 1  
 FT NON\_TER 194  
 FT SEQUENCE 194 AA; 20890 MW; 3AA3D947D187AF9A CRC64;

Query Match 18.1%; Score 247.5; DB 6; Length 194;  
 Best Local Similarity 30.9%; Pred. No. 1,7e-14;  
 Matches 60; Conservative 36; Mismatches 71; Indels 27; Gaps 6;

OY 54 GP-----PGPPG-----GIPGNHNGNNGNNGATGHEGAKGKGDGDC---LGPGRGRCO- 100  
 DB 1 GPVLLPLPKGACGCGMAGIPGHPGHNCTPGRDGKGDTGEGEGKGDGLVGPKGDTGET 60  
 OY 101 --HGPKGEGYPIPEL-----QIAFMASLATHFSNONGIIFSSVETNIGNEF 148  
 DB 61 GVTGVEGPRGPGTGRGGEPEASAVYHRSAPSVGLSESLITYVNPPIRTKIFYNLQNH 120  
 OY 149 DVWTRFGAPVSGVFEFTFSNMKHEDEVEYVYLLMHNGTIVSMYSYEKKGSDTSSNHA 208  
 DB 121 DGTGKGFHCNIPGLYFYSHTIVY--LKDVKSLYKKDKAMLETYDQYQEKHVDQASGV 178  
 OY 209 VLKLAKGDEVLMR 222

Db 179 LHLFVGGQVWLVQ 192

## RESULT 15

09DCM6 PRELIMINARY; PRT: 245 AA.

AC 09DCM6;

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE Complement component 1, q subcomponent, alpha polypeptide.

GN C1QA.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=KIDNEY;

RA MEDLINE=21085660; Pubmed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher R., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,

RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,

RA Hayashizaki Y.;

RT \*Functional annotation of a full-length mouse cDNA collection.\*;

RL Nature 409:685-690(2001).

RN [2]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

EMBL: AK002655; BAB2262.1; -

DR EMBL: BC002086; AA02086.1; -

DR MGI:88223; C1qa.

DR InterPro: IPR001073; C1q.

DR InterPro: IPR000087; Collagen.

DR Pfam: PF00386; C1q; 1.

DR Pfam: PF01391; Collagen; 1.

DR PRINTS: PRO0007; COMPLEMENTC1Q.

DR SMART: SM00110; C1Q; 1.

DR PROSITE: PS01113; C1Q; 1.

DR SEQUENCE 245 AA; 25974 MW; 41C2066D49592020 CRC64;

Query Match 17 5%; Score 239.5; DB 11; Length 245;

Best Local Similarity 33.2%; Pred. No. 1.2e-13;

Matches 71; Conservative 26; Mismatches 94; Indels 23; Gaps 7;

QY 51 GYGGPPGPPGPGIPGNHGNNGNNGATG-HEGAKGKGDKGD-----LGP 94

DB 31 GKDGAPGPGPGPGPKGKGEGGPGAGIRGIRGFGKDPGSGPPGKPGNVGLPGPSGP 90

QY 95 RGERGQHGPKGEGKIPG-IPPELQIAFMASLATHFSNONGSIIFSSVETNIGNFPDWTG 153

DB 91 LGDSGPGGLGKGVGNPCNIRPDPAFSAIRQNPMTLGNV-VIPDKYVLTNQESPYQNHGTG 149

QY 154 RFGAPVSGVVEFTFSMKHEDVEVYVYLMHNG--NTVFSMTSEYEMKCKSDTSSNHAVALK 211

DB 150 RFGCAVVGFTYFNFQVTSKMDL-CLFTKSSSGGQPRDLSLFSNTNKGFLFOVLAGTVLQ 208

QY 212 LAKGDEWLRL--NGALHGDHQRSTFAGFLIF 243

DB 209 LRRGDEWIERKDPKRGRIYOGTEADSIFFSGFLIF 242

Search completed: January 15, 2003, 19:39:47

Job time : 94 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OH protein - protein search, using sw model

Run on: January 15, 2003, 19:37:15 ; Search time 244 Seconds  
(without alignments)  
20.041 Million cell updates/sec

Title: US-10-036-041-2

Perfect score: 1367  
Sequence: 1 MLMQLIYMWLALFLPFC.....LHGDRHFRFAGFLLETK 246

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_AA:\*

- 1: /cgn2-6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 2: /cgn2-6/ptodata/1/pubpaa/PCIT\_NEW\_PUB.pep:\*
- 3: /cgn2-6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2-6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2-6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2-6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 7: /cgn2-6/ptodata/1/pubpaa/PCITUS\_PUBCOMB.pep:\*
- 8: /cgn2-6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2-6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 10: /cgn2-6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2-6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 12: /cgn2-6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*
- 13: /cgn2-6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 14: /cgn2-6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
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| 1          | 1367  | 100.0       | 246    | 9  | US-10-036-041-2   |
| 2          | 1367  | 100.0       | 246    | 9  | US-10-035-855-2   |
| 3          | 1367  | 100.0       | 246    | 12 | US-10-036-342-2   |
| 4          | 294   | 21.5        | 247    | 10 | US-09-776-876-4   |
| 5          | 294   | 21.5        | 247    | 10 | US-09-758-055-4   |
| 6          | 294   | 21.5        | 247    | 10 | US-09-909-547-4   |
| 7          | 293.5 | 21.5        | 244    | 9  | US-09-911-176B-8  |
| 8          | 293.5 | 21.5        | 244    | 10 | US-09-776-976-6   |
| 9          | 293.5 | 21.5        | 244    | 10 | US-09-758-055-6   |
| 10         | 293.5 | 21.5        | 244    | 10 | US-09-909-547-6   |
| 11         | 293   | 21.4        | 247    | 10 | US-09-776-976-2   |
| 12         | 293   | 21.4        | 247    | 10 | US-09-758-055-2   |
| 13         | 293   | 21.4        | 247    | 10 | US-09-909-547-2   |
| 14         | 290.5 | 21.3        | 259    | 9  | US-09-992-598-47  |
| 15         | 290.5 | 21.3        | 259    | 9  | US-09-988-293A-47 |
| 16         | 290.5 | 21.3        | 259    | 9  | US-09-988-735-47  |
| 17         | 290.5 | 21.3        | 259    | 9  | US-09-990-444-47  |
| 18         | 290.5 | 21.3        | 259    | 9  | US-09-989-730-47  |
| 19         | 290.5 | 21.3        | 259    | 9  | US-09-990-436-47  |

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|----|-------|------|-----|----|-------------------|-------------------|
| 20 | 290.5 | 21.3 | 259 | 9  | US-09-991-181-47  | Sequence 47, Appl |
| 21 | 290.5 | 21.3 | 259 | 9  | US-09-993-687-47  | Sequence 47, Appl |
| 22 | 290.5 | 21.3 | 259 | 9  | US-09-989-734-47  | Sequence 47, Appl |
| 23 | 290.5 | 21.3 | 259 | 9  | US-09-997-653-47  | Sequence 47, Appl |
| 24 | 290.5 | 21.3 | 259 | 9  | US-10-174-590-62  | Sequence 62, Appl |
| 25 | 290.5 | 21.3 | 259 | 9  | US-10-176-758-62  | Sequence 62, Appl |
| 26 | 290.5 | 21.3 | 259 | 10 | US-09-989-722-47  | Sequence 47, Appl |
| 27 | 290.5 | 21.3 | 259 | 10 | US-09-989-723-47  | Sequence 47, Appl |
| 28 | 290.5 | 21.3 | 259 | 10 | US-09-989-727-47  | Sequence 47, Appl |
| 29 | 290.5 | 21.3 | 259 | 10 | US-09-989-731-47  | Sequence 47, Appl |
| 30 | 290.5 | 21.3 | 259 | 10 | US-09-989-732-47  | Sequence 47, Appl |
| 31 | 290.5 | 21.3 | 259 | 10 | US-09-991-073-47  | Sequence 47, Appl |
| 32 | 290.5 | 21.3 | 259 | 10 | US-09-990-442-47  | Sequence 47, Appl |
| 33 | 290.5 | 21.3 | 259 | 10 | US-09-991-163-47  | Sequence 47, Appl |
| 34 | 290.5 | 21.3 | 259 | 10 | US-09-993-604-47  | Sequence 47, Appl |
| 35 | 290.5 | 21.3 | 259 | 10 | US-09-990-456-47  | Sequence 47, Appl |
| 36 | 290.5 | 21.3 | 259 | 10 | US-09-989-721-47  | Sequence 47, Appl |
| 37 | 290.5 | 21.3 | 259 | 12 | US-10-052-586-62  | Sequence 62, Appl |
| 38 | 290.5 | 21.3 | 278 | 10 | US-09-799-777-35  | Sequence 35, Appl |
| 39 | 289.5 | 21.2 | 247 | 9  | US-09-911-176B-3  | Sequence 3, Appl  |
| 40 | 287   | 21.0 | 746 | 9  | US-09-854-133-185 | Sequence 185, App |
| 41 | 273   | 20.0 | 746 | 10 | US-09-738-973-185 | Sequence 185, App |
| 42 | 273   | 20.0 | 746 | 10 | US-09-944-413-42  | Sequence 42, Appl |
| 43 | 264.5 | 19.3 | 243 | 9  | US-09-944-403-42  | Sequence 42, Appl |
| 44 | 264.5 | 19.3 | 243 | 9  | US-09-944-403-42  | Sequence 42, Appl |
| 45 | 264.5 | 19.3 | 243 | 9  | US-09-944-896-42  | Sequence 42, Appl |

#### ALIGNMENTS

RESULT 1  
US-10-036-041-2  
Sequence 2, Application US/10036041  
Publication No. US2002019251A1  
GENERAL INFORMATION:  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3030R1C8  
CURRENT APPLICATION NUMBER: US/10/036,041  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/112514  
PRIOR FILING DATE: 1998-12-15  
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PRIOR APPLICATION NUMBER: PCT/US00/05841  
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PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/17800  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: PCT/US01/19692  
PRIOR FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: PCT/US01/21066  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 80  
SEQ ID NO 2  
LENGTH: 246  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-036-041-2  
Query Match 100.0%; Score 1367; DB 9; Length 246;  
Best Local Similarity 100.0%; Pred. No. 9.9e-112;  
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLMRQLYMWLLALFPLPFCICQDEYNESPQTGGLPPDCSKCHGDSYFRGOGPPGPG 60  
D6 1 MLMRQLYMWLLALFPLPFCICQDEYNESPQTGGLPPDCSKCHGDSYFRGOGPPGPG 60  
QY 61 PPGIPGNHGNNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKEGYPGIPPELQIAF 120  
D6 61 PPGIPGNHGNNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKEGYPGIPPELQIAF 120  
QY 121 MASLATHPSNONGSILFSSVETNIGNEFDWTRGFGAPVSGVYFETSMKHDEVEEYV 180  
D6 121 MASLATHPSNONGSILFSSVETNIGNEFDWTRGFGAPVSGVYFETSMKHDEVEEYV 180  
QY 181 YLMHNGTVFSMYSYEMKKGSDTSSNHAIVLKLAKGDEWLMRGALGHORESTFAGF 240  
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QY 241 LLEFETK 246  
D6 241 LLEFETK 246  
RESULT 2  
US-10-035-855-2  
Sequence 2, Application US/10035855  
Publication No. US20030008348A1  
GENERAL INFORMATION:  
APPLICANT: Desnoyers, Luc  
APPLICANT: Paton, Dan L.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Wood, William L.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3030RIC4  
CURRENT APPLICATION NUMBER: US/10/035,855  
CURRENT FILING DATE: 2001-12-26  
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PRIOR FILING DATE: 1998-05-15  
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PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: PCT/US00/14042  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: PCT/US00/23522  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/17800  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: PCT/US01/19692  
PRIOR FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: PCT/US01/21066  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 80  
SEQ ID NO 2  
LENGTH: 246  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-035-855-2

Query Match 100.0%; Score 1367; DB 9; Length 246;  
Best Local Similarity 100.0%; Pred. No. 9.9e-112;  
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMRLIYQWLLALFPLPCQDEYMESPTGGLPPDCSKCHDYSRGTQGPPEPG 60  
DB 1 MIMRLIYQWLLALFPLPCQDEYMESPTGGLPPDCSKCHDYSRGTQGPPEPG 60  
QY 61 PPGIGNNGNNGNNGATGHEGAKGEGDKGDLGPRGERGQHPKGEKGPGLPELQIAF 120  
DB 61 PPGIGNNGNNGNNGATGHEGAKGEGDKGDLGPRGERGQHPKGEKGPGLPELQIAF 120  
QY 121 MASLATHFSNONGIIFSSVETNIGNFDVMTGRGAPVSGVYFFTFSMKHEDVEEYV 180  
DB 121 MASLATHFSNONGIIFSSVETNIGNFDVMTGRGAPVSGVYFFTFSMKHEDVEEYV 180  
QY 181 YLMHNGNTVFSWYSYEMKSDTSNHAVALKAKGDEYWLRMGNGALHGDHORESTFAGF 240  
DB 181 YLMHNGNTVFSWYSYEMKSDTSNHAVALKAKGDEYWLRMGNGALHGDHORESTFAGF 240  
QY 241 LLEFETK 246  
DB 241 LLEFETK 246

RESULT 3  
US-10-036-342-2  
Sequence 2, Application US/10036342  
Patent No. US2002090681A1  
GENERAL INFORMATION:  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Guiney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3030R1C5

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CURRENT APPLICATION NUMBER: US/10/036,342
PRIOR FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114140
PRIOR FILING DATE: 1998-12-23
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PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/116843
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/125774
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/125778
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/125826
PRIOR FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 60/127035
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/127706
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/129122
PRIOR FILING DATE: 1999-04-13
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PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
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PRIOR FILING DATE: 1999-04-27
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PRIOR FILING DATE: 1999-04-27
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PRIOR FILING DATE: 1999-05-04
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PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: 60/132383
PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138166
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 60/144791
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/146970
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 09/311832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/644848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 09/747259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/816744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/854208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/854280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/874503
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/869599

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PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/908,827
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US99/10733
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US99/28551
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30720
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/23322
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
ORGANISM: Homo Sapien
US-10-036-342-2

Query Match      100.0%; Score 1367; DB 12; Length 246;
Best Local Similarity 100.0%; Pred. No. 9,9e-112;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MLMROLIYQMLLAFPLPFCICODEYMSPTGGLPPDCSKCHGDYSEFRGYOGPPGPG 60
Db      1  MLMROLIYQMLLAFPLPFCICODEYMSPTGGLPPDCSKCHGDYSEFRGYOGPPGPG 60
QY      61  PPGIPGNHGNNGNNGATGHEGAKGEGDKGDLGPRGERGQHPKGEKGYPGIPELQIAF 120
Db      61  PPGIPGNHGNNGNNGATGHEGAKGEGDKGDLGPRGERGQHPKGEKGYPGIPELQIAF 120
QY      121  MASLATHFSNQNSGIIITSSVETNIGNEFDVVTGRRFGAPVSCVYFFTFESMKHEDVEEYV 180
Db      121  MASLATHFSNQNSGIIITSSVETNIGNEFDVVTGRRFGAPVSCVYFFTFESMKHEDVEEYV 180
QY      181  YLMHNGTFSMTSEYKKGKSDTSSNNAVLKLAGDEWMLRMGALHGDHORESTFAGF 240
Db      181  YLMHNGTFSMTSEYKKGKSDTSSNNAVLKLAGDEWMLRMGALHGDHORESTFAGF 240
QY      241  LLEFETK 246
Db      241  LLEFETK 246

RESULT 4
US-09-776-976-4
; Sequence 4, Application US/09776976
; Patent No. US20020037849A1
; GENERAL INFORMATION:
; APPLICANT: Friedbis, Joachim

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: APPLICANT: Erickson, Mary Ruth
: APPLICANT: Yen, Frances
: TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass
: FILE REFERENCE: 76, US4, REG.
: CURRENT APPLICATION NUMBER: US/09/776, 976
: PRIOR FILING DATE: 2001-02-05
: PRIOR APPLICATION NUMBER: US 09/758, 055
: PRIOR FILING DATE: 2001-01-10
: PRIOR APPLICATION NUMBER: US 60/176, 228
: PRIOR FILING DATE: 2000-01-14
: PRIOR APPLICATION NUMBER: US 60/198, 087
: PRIOR FILING DATE: 2000-04-13
: PRIOR APPLICATION NUMBER: US 60/299, 881
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: Patent.pm
: SEQ ID NO 4
: LENGTH: 247
: TYPE: PRT
: ORGANISM: mus musculus
: US-09-776-976-4

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Query Match      21.5% Score 294; DB 10; Length 247;
Best Local Similarity 31.5%; Pred. No. 1.5e-18;
Matches 81; Conservative 40; Mismatches 102; Indels 34; Gaps 9;

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OY 6 LLYWOLALFFLPCLCODEYVESPOTG--LPPDCSKCHGDYSPRGQGPFGPPG 63
   1: 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 2 LLLQALLFLILLP-SHAEDDYTTTELAPALVPPKGTCA-----GMA-----GIPG 48
OY 64 IPGNHNGNNGCATGHEGAKGKGDGLGPRGER---GQHPKGEKGYPGIPE----- 115
   1111111111111111111111111111111111111111111111111111111
DB 49 HPGHNGTGRDRDGTGPKGKGDAGLLGPKGETGDMTGAEGRGPPTGPKRKGEPG 108
   1111111111111111111111111111111111111111111111111111111
OY 116 -----LQIAFNASLATHFNSNONGIIFSSVETNIGNFEDVMTGRGAPVSGVYFTFSMM 170
   1111111111111111111111111111111111111111111111111111111
DB 109 EAAVYRSASFVSGLETRVYVNPVPIRFTKIFYNQONHNDGSGTKFCNIPGLYFSYHIT 168
   1111111111111111111111111111111111111111111111111111111
OY 171 KHEDEEYVYVLMHNGNTVFSMYSTEMKGSJDTSSNHAVLKLAKGDEWLRLM-GNG---A 226
   1111111111111111111111111111111111111111111111111111111
DB 169 VY--MKDVKVSLEFKKDKAVLFTYDQYQEKNVQASGSVLLHLEVGDQWLQYVGDDHNG 226
   1111111111111111111111111111111111111111111111111111111
OY 227 LHGDRHGFSTFAGFLIF 243
   1111111111111111111111111111111111111111111111111111111
DB 227 LYADVNDSTFTGFLY 243

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RESULT 5
US-09-758-055-4
: Sequence 4, Application US/09758055
: Patent No. US20020058617A1
: GENERAL INFORMATION:
: APPLICANT: Fruebis, Joachim
: APPLICANT: Erickson, Mary Ruth
: APPLICANT: Yen, Frances
: TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass
: FILE REFERENCE: 76, US4, REG.
: CURRENT APPLICATION NUMBER: US/09/758, 055
: PRIOR FILING DATE: 2001-01-10
: PRIOR APPLICATION NUMBER: US 60/176, 228
: PRIOR FILING DATE: 2000-01-14
: PRIOR APPLICATION NUMBER: US 60/198, 087
: PRIOR FILING DATE: 2000-04-13
: PRIOR APPLICATION NUMBER: US 60/299, 881
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: Patent.pm
: SEQ ID NO 4
: LENGTH: 247
: TYPE: PRT
: ORGANISM: mus musculus

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US-09-758-055-4
Query Match      21.5% Score 294; DB 10; Length 247;
Best Local Similarity 31.5%; Pred. No. 1.5e-18;
Matches 81; Conservative 40; Mismatches 102; Indels 34; Gaps 9;

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OY 6 LLYWOLALFFLPCLCODEYVESPOTG--LPPDCSKCHGDYSPRGQGPFGPPG 63
   1: 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 2 LLLQALLFLILLP-SHAEDDYTTTELAPALVPPKGTCA-----GMA-----GIPG 48
OY 64 IPGNHNGNNGCATGHEGAKGKGDGLGPRGER---GQHPKGEKGYPGIPE----- 115
   1111111111111111111111111111111111111111111111111111111
DB 49 HPGHNGTGRDRDGTGPKGKGDAGLLGPKGETGDMTGAEGRGPPTGPKRKGEPG 108
   1111111111111111111111111111111111111111111111111111111
OY 116 -----LQIAFNASLATHFNSNONGIIFSSVETNIGNFEDVMTGRGAPVSGVYFTFSMM 170
   1111111111111111111111111111111111111111111111111111111
DB 109 EAAVYRSASFVSGLETRVYVNPVPIRFTKIFYNQONHNDGSGTKFCNIPGLYFSYHIT 168
   1111111111111111111111111111111111111111111111111111111
OY 171 KHEDEEYVYVLMHNGNTVFSMYSTEMKGSJDTSSNHAVLKLAKGDEWLRLM-GNG---A 226
   1111111111111111111111111111111111111111111111111111111
DB 169 VY--MKDVKVSLEFKKDKAVLFTYDQYQEKNVQASGSVLLHLEVGDQWLQYVGDDHNG 226
   1111111111111111111111111111111111111111111111111111111
OY 227 LHGDRHGFSTFAGFLIF 243
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DB 227 LYADVNDSTFTGFLY 243

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RESULT 6
US-09-909-547-4
: Sequence 4, Application US/09909547
: Patent No. US20020091080A1
: GENERAL INFORMATION:
: APPLICANT: Fruebis, Joachim
: APPLICANT: Erickson, Mary Ruth
: APPLICANT: Yen, Frances
: TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass
: FILE REFERENCE: 76, US6, CIP
: CURRENT APPLICATION NUMBER: US/09/909, 547
: PRIOR FILING DATE: 2001-07-19
: PRIOR APPLICATION NUMBER: US 09/776, 976
: PRIOR FILING DATE: 2001-02-05
: PRIOR APPLICATION NUMBER: US 09/758, 055
: PRIOR FILING DATE: 2001-01-10
: PRIOR APPLICATION NUMBER: US 60/299, 881
: PRIOR FILING DATE: 2000-09-01
: PRIOR APPLICATION NUMBER: US 60/198, 087
: PRIOR FILING DATE: 2000-04-13
: PRIOR APPLICATION NUMBER: US 60/176, 228
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: Patent.pm
: SEQ ID NO 4
: LENGTH: 247
: TYPE: PRT
: ORGANISM: mus musculus
: US-09-909-547-4
Query Match      21.5% Score 294; DB 10; Length 247;
Best Local Similarity 31.5%; Pred. No. 1.5e-18;
Matches 81; Conservative 40; Mismatches 102; Indels 34; Gaps 9;

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OY 208 AVLKAKDEVLRLM-GNG---ALHGDHORESTFAGELLF 243  
 Db 201 VLLHLEVGDDQVWLQYGGEGERNGLYADNDNDSTFTGFLLY 240

## RESULT 10

US-09-909-547-6  
 ; Sequence 6, Application US/09909547  
 ; Patent No. US20020091080A1

GENERAL INFORMATION:

APPLICANT: Fruebis, Joachim  
 APPLICANT: Erickson, Mary Ruth  
 APPLICANT: Yen, Frances

TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass  
 FILE REFERENCE: 76. US6.CIP

CURRENT APPLICATION NUMBER: US/09/909,547  
 CURRENT FILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: US 09/776,976  
 PRIOR FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: US 09/758,055  
 PRIOR FILING DATE: 2001-01-10

PRIOR APPLICATION NUMBER: US 60/299,881  
 PRIOR FILING DATE: 2000-09-01

PRIOR APPLICATION NUMBER: US 60/198,087  
 PRIOR FILING DATE: 2000-04-13

PRIOR APPLICATION NUMBER: US 60/176,228  
 PRIOR FILING DATE: 2000-01-14

NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: Patent.pm

SEQ ID NO 6  
 LENGTH: 244

TYPE: PRT  
 ORGANISM: Homo sapiens

US-09-909-547-6

Query Match 21.5%; Score 293.5; DB 10; Length 244;  
 Best Local Similarity 34.5%; Pred. No. 1.7e-18;  
 Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

OY 53 QGP-----PGPPGP-----PGIPGNHNGNNGANGHEGAKGDKGD---LGPR---GE 97  
 Db 23 QGPGLVLPFGACTGMAGIPGHGHNHNGNNGANGHEGAKGDKGD---LGPR---GE 82  
 OY 98 RGOGPKGKGYPGI-----PPE-----LQIAFMASLATHFSNONGIIESSVENINCNF 147  
 Db 83 TGVGAEPRPFGPGIQQKKGEGEGAYYKSAFSGVGLTETVTPMPPIRFKIRFYNOQNH 142  
 OY 148 FDMVTRGAFVSGVYFTFSMKRHEDEYVYVLMHNGNTVFSMYEMKKSPTSNNH 207  
 Db 143 YDGTGKFNHNPGLYFAVHITVY--MKDVKVSLEFKKDKAMLFYDDYQENNDQASGS 200  
 OY 208 AVLKAKDEVLRLM-GNG---ALHGDHORESTFAGELLF 243  
 Db 201 VLLHLEVGDDQVWLQYGGEGERNGLYADNDNDSTFTGFLLY 240

## RESULT 11

US-09-776-976-2  
 ; Sequence 2, Application US/09776976  
 ; Patent No. US20020037849A1

GENERAL INFORMATION:

APPLICANT: Fruebis, Joachim  
 APPLICANT: Erickson, Mary Ruth  
 APPLICANT: Yen, Frances

TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass  
 FILE REFERENCE: 76. US4. REG

CURRENT APPLICATION NUMBER: US/09/776,976  
 CURRENT FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: US 09/758,055  
 PRIOR FILING DATE: 2001-01-10

PRIOR APPLICATION NUMBER: US 60/176,228  
 PRIOR FILING DATE: 2000-01-14  
 PRIOR APPLICATION NUMBER: US 60/198,087  
 PRIOR FILING DATE: 2000-04-13  
 PRIOR APPLICATION NUMBER: US 60/299,881  
 PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: Patent.pm

SEQ ID NO 2  
 LENGTH: 247

TYPE: PRT  
 ORGANISM: mus musculus

US-09-776-976-2

Query Match 21.4%; Score 293; DB 10; Length 247;  
 Best Local Similarity 31.2%; Pred. No. 1.9e-18;  
 Matches 81; Conservative 40; Mismatches 99; Indels 40; Gaps 10;

OY 6 LIYWQALLFPLPCLCODEYMESPTGG--LPPDCSKCHDYSFRGYOGPPGPPG 63  
 Db 2 LLLQALLFLFLIP-SHAEDVTTTEELAPALVPPPKGTCA-----GMA-----G 45  
 OY 64 IPGNHNGNNGANGHEGAKGDKGD---LGPRGER---GQHPKKGKYPGIPPE-- 115  
 Db 46 IPGSHNGTGPGRDGTPEKGEKGDGLGPKGETGVDMGAEGRPGFPGPKRG 105  
 OY 116 -----LQIAFMASLATHFSNONGIIESSVENINCNFDMVTRGAFVSGVYFTF 167  
 Db 106 EPGEAAYYKSGFSVGLTETVTPMPPIRFKIRFYNOQNHNSGKFKYCNPSGLYFSY 165  
 OY 168 SMKRHEDEYVYVLMHNGNTVFSMYEMKKSPTSNNHVLKAKDEVLRLM-GNG- 225  
 Db 166 HITVY--MKDVKVSLEFKKDKAMLFYDDYQENNDQASGSVLLHLEVGDDQVWLQYGGSD 223  
 OY 226 --ALHGDHORESTFAGELLF 243  
 Db 224 HNGLYADNDNDSTFTGFLLY 243

## RESULT 12

US-09-758-055-2  
 ; Sequence 2, Application US/09758055  
 ; Patent No. US20020058617A1

GENERAL INFORMATION:

APPLICANT: Fruebis, Joachim  
 APPLICANT: Erickson, Mary Ruth  
 APPLICANT: Yen, Frances

TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass  
 FILE REFERENCE: 76. US4. REG

CURRENT APPLICATION NUMBER: US/09/758,055  
 CURRENT FILING DATE: 2001-01-10

PRIOR APPLICATION NUMBER: US 60/176,228  
 PRIOR FILING DATE: 2000-01-14

PRIOR APPLICATION NUMBER: US 60/198,087  
 PRIOR FILING DATE: 2000-04-13

PRIOR APPLICATION NUMBER: US 60/299,881  
 PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: Patent.pm

SEQ ID NO 2  
 LENGTH: 247

TYPE: PRT  
 ORGANISM: mus musculus

US-09-758-055-2

Query Match 21.4%; Score 293; DB 10; Length 247;  
 Best Local Similarity 31.2%; Pred. No. 1.9e-18;  
 Matches 81; Conservative 40; Mismatches 99; Indels 40; Gaps 10;

OY 6 LIYWQALLFPLPCLCODEYMESPTGG--LPPDCSKCHDYSFRGYOGPPGPPG 63  
 Db 2 LLLQALLFLFLIP-SHAEDVTTTEELAPALVPPPKGTCA-----GMA-----G 45



[illegible]

PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
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PRIOR FILING DATE: 1998-06-10  
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PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
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PRIOR FILING DATE: 1998-06-17  
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PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090254  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349

PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090435  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
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PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 21.3%; Score 290.5; DB 9; Length 259;  
Best Local Similarity 28.8%; Pred. No. 3.3e-18;  
Matches 78; Conservative 34; Mismatches 96; Indels 63; Gaps 10;

QY 9 WQALLFLPFLCQDEYMSPTGSLPPQSKCC-----HGDYS 48  
DB 10 WAALLFLPL--MCEIRNVELTFDRAVASGQRCQDSEDLDPANVSSASSSGRPHALPE 66  
QY 49 FRGY-----QGPFGPPGPGIPGNNHNGNNGATGHEGAKGEGKGDGGLGPRGERQHG 102  
DB 67 IRPYINTILKGDGKDPGPRGLGMYKREBPQGEPRQSGKD----- 109  
QY 103 PRKEGYPGIPELQIAFMA-----SLATHFSNONSIIIFSSVETNIGNFEDVWTGRFGA 157  
DB 110 -KSEMSPGAP--COKRFFAFSVGRKTAHSGEDFCITLFEFVNVLDGCGFDMATGQFAA 166

OY 158 PVSQVFEFESMKHE-DVEEYVYVLMHNGTFSMYSKMGKSDTSSNNAVLKAKD 216  
Db 167 PLRITFFSLAV--HSWRYKTTYHIMNOKEAVILTA-QPSERSIMQOSVMDLAYGD 223  
OY 217 EVWLRM-----NGALHGDHOREFSTFAGFIL 242  
Db 224 RWWYRLFRRORENAIYSNDFPTITFSGHLI 254

RESULT 15  
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Sequence 47, Application US/09989293A  
Patent No. US20020177164A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerilsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PLC66  
CURRENT APPLICATION NUMBER: US/09/989,293A  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 21.3%; Score 290.5; DB 9; Length 259;  
Best Local Similarity 28.8%; Pred. No. 3.3e-18;  
Matches 78; Conservative 34; Mismatches 96; Indels 63; Gaps 10;

9 WQALAFPLPCICQDEYMESPTGTGGLPPDCSKC-----HGDIS 48

DB 10 WALLLFTL---MCEIRWELTFEDRAVAGCCORCCDSEDDPLDPAHVSSASSGRRHALPE 66  
QY 49 FRGY-----OGPPGPPGPGIGNHNNGNNGATGHECAKGEKGDKGLGPRGERGQHG 102  
DB 67 IRPYINITILKDKRDPGPMGLPGYMGREGPGEGEPQOSKGD----- 109  
QY 103 PKGEGYPGIPELQIAFMA-----SLATHFSNONGIIFSSVEETNIGNFDPVMTGRFGA 157  
DB 110 -KGEWGSPGAP--CQKRFPAFSVGRKTLHSGEDFQTLLEFVFNLDGCFDMATGQFAA 166  
QY 158 PVSQYVFTFTSMKHE-DVEEYVYVLMHNGNTVFSMYSTEMKGSQDTSNNAVLKLAKD 216  
DB 167 PLRGYFFSLNV--HSWNYKETVYVIMHNOKEAVILYA-QPSERSIMOSQSVMLDLAYGD 223  
QY 217 EYVLRM-----GNGALHGDHGFSTFAGPL 242  
DB 224 RWVRLFKRRENAIYSNDPTIYITFSGLI 254

Search completed: January 15, 2003, 19:45:53  
Job time : 245 secs

The invention relates to novel nucleic acid sequences derived from rat dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences AAZ61606-261832 represent cDNA sequences derived from several mouse, rat or human skin cell types. Sequences AAZ61606-261649, AAZ61125-261765, AAZ61802-261811 and AAZ61826 encode proteins with an N-terminal signal sequence, indicating that the proteins are secreted. Sequences AAZ61650-261668, AAZ61766-261780, AAZ61812-261817 and AAZ61827-261829 encode proteins with one or more putative transmembrane domains.

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| Score:                | 131.00   |
| Percent Similarity:   | 97.15%   |
| Best local Smilarity: | 95.93%   |
| Query Match:          | 95.90%   |
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|                       |          |
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| Conservative:         | 3        |
| Mismatches:           | 7        |
| Indels:               | 0        |
| Gaps:                 | 0        |

US-10-036-041-2 (1-246) x AAZ61633 (1-1123)

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | MetLeuTrpArgGlnLeuLeuLeuLeuTyrTrpGlnLeuLeuLeuLeuPheLeuLeuProPheCys | 20  |
| Db | 180 | ATGCTCAGAGAGACGCTCGTGGTGGCACCCTGCTGGCTTTGCTTTTCTCCCATTTTGC         | 239 |
| QY | 21  | LeuCysGlnAspGluTyrMetGlnSerProGlnThrGlyGlyLeuProProAspCysSer       | 40  |
| Db | 240 | CTGTGTCAGATGATCATCATGAGTCTCCACAAAGCTGAGAGACTGCCCCAGACTGCAGC        | 299 |
| QY | 41  | LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly       | 60  |
| Db | 300 | AAGGTGTCCATGGAGATATGATGATTCGCTGGTTACCAAGGGCCCCCTGGAGCCCCAGGT       | 359 |
| QY | 61  | ProProGlyIleProGlyAsnHisGlyAsnAsnGlnYasnAsnGlyAlaThrGlnHisGlu      | 80  |
| Db | 360 | CCTCTGGCATTCACAGGAACATGGAACATGAAATACGAGACCTATGGCCACAGAA            | 419 |
| QY | 81  | GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln       | 100 |
| Db | 420 | GGGGCCAAAGCGGTGAAGAAAGACAAAGGCGACCTGGGGCCCTCGAGGGGAACGGGGCAG       | 479 |
| QY | 101 | HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe       | 120 |
| Db | 480 | CATGGCCCCAAAGATAGAAAGGATACCCAGGGGTGGCCACAGAGCTGCAGATGGCTTC         | 539 |
| QY | 121 | MetaSerLeuLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal      | 140 |
| Db | 540 | ATGGCTTCTTAGGAGACTCACTTACGACATCAAGAAAGTGCGATTATCTTCACAGAGT         | 599 |
| QY | 141 | GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer       | 160 |
| Db | 600 | GAGACCAACATTGGAAACCTTCTTGATGCTCATGACTGCTGATTTGGGGCCCCCGTATCA       | 659 |
| QY | 161 | GlyValTyrPhePheThrPheSerMetMetLysHisGlnAspValGluGluValTyrVal       | 180 |
| Db | 660 | GGCGGTATTTCTTCACCTTCAGCATATCAAGCATAGAGACGTGGAGGAAGGTATGTG          | 719 |
| QY | 181 | TyrLeuMetHisAsnGlyAsnThrValPheSerMetLysSerTyrGluMetLysGlyLys       | 200 |
| Db | 720 | TACCTTATGCACATATGGTGAACACGCGTGTTCAGCATGTACAGCTATGAACAAAGGAGAAA     | 779 |
| QY | 201 | SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPheLeu    | 220 |

| ID | AAZ61730 | standard; cDNA; 1123 BP |
|----|----------|-------------------------|
|    |          |                         |

AC AA261730;  
yy

|    |             |               |
|----|-------------|---------------|
| DT | 27-MAR-2000 | (first entry) |
| XX |             |               |

DE cDNA encoding rat skin cell secreted protein, SEQ ID NO:203.  
XX

KW embryonic skin cell: keratinocyte stem cell: transit amplifying cell]

angiogenesis; tumour vascularisation; growth disorder;  
KW

KW anti-inflammatory; cytostatic; neuroprotective; vulnery; ss

OS Ratus sp.

PN W09955865-A1.

PD 04-NOV-1999

PF 29-APR-1999; 99WO-NZ00051.  
YY

|    |              |               |
|----|--------------|---------------|
| PR | 29-APR-1998; | 98US-0069726. |
| PR | 09-NOV-1998. | 98US-0188930  |

PA (GENE-) GENESTS RES & DEV CORP LTD  
XX

XX Strachan L., Sleeman M., Watson J.D., Orust R., Kumble A., Morrison J.G.

WPI: 2000-072177/06

XX F-PSDB; AA1 / 0023.

PT  
I  
however polymericides useful for the treatment of various conditions including wounds and cancer -

PS Claim 1; Page 137; 235pp;. English

CC The invention relates to novel nucleic acid sequences derived from rat  
CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,  
CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying  
CC cells. Polypeptides of the invention may be used to treat inflammation,  
CC cancer and neurological diseases. The proteins may be used to stimulate  
CC the growth and motility of keratinocytes, to inhibit the growth of  
CC cancer cells, to modulate angiogenesis and tumour vascularisation, to  
CC modulate skin inflammation, to modulate epithelial cell growth and to  
CC inhibit binding of HIV-1 to leukocytes. The invention may also be used  
CC to treat growth and developmental defects, skin wounds and hair follicle  
CC disorders. Sequences AA261606-261832 represent cDNA sequences derived  
CC from several mouse, rat or human skin cell types. Sequences  
CC AA261606-261649, AA261725-261785, AA261802-261811 and AA261826 encode  
CC proteins with an N-terminal signal sequence, indicating that the proteins  
CC are secreted. Sequences AA261650-261668, AA261766-261780, AA261812-261817  
CC and AA261827-261829 encode proteins with one or more putative  
CC transmembrane domains.

Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other.

|                   |          |         |      |
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| Alignment Scores: | 3.36e-95 | Length: | 1123 |
| Pred. No.:        |          |         |      |

5

US-10-036-041-2 (1-246) x AA261730 (1-1123)

KM inflammation; neurological disease; ss.  
OS Rattus sp.  
PN WO20069884-A2.  
XX  
XX PD 23-NOV-2000.  
XX PF 15-MAY-2000; 2000WO-NZ00075.  
XX PR 14-MAY-1999; 99US-0312283.  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
XX PA Watson JD, Strachan L, Onurst R, Sleeman M, Kumble KD, Murison JG;  
PI WPI: 2001-007495/01.  
XX DR P-PSTDB: AAB55908.  
XX PS New isolated polynucleotide used in the identification of genetic  
PT disorders and encoding polypeptides used for treating inflammatory  
PT disease, cancer and neurological diseases -  
XX Claim 1; Page 87; 352pp; English.

The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV) 1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of oligonucleotides for examining expression patterns.

Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other:

| Alignment Scores:      |          |               |      |
|------------------------|----------|---------------|------|
| Pred. NO.:             | 3,36e-95 | Length:       | 1123 |
| Score:                 | 1311.00  | Matches:      | 236  |
| Percent Similarity:    | 97.15%   | Conservative: | 3    |
| Best Local Similarity: | 95.93%   | Mismatches:   | 7    |
| Query Match:           | 95.90%   | Indels:       | 0    |
| DB:                    | 22       | Gaps:         | 0    |

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US-10-036-041-2 (1-246) x AAC99566 (1-1123)
QY      1 MetLeuTPrArgInLeuIleTyTTPGInLeuAlaLeuPhheLeuProPhcys 20
       ||||| |||||||:||||| ||||||| ||||||| ||||||| |||||||
Db     180 ATGTCTCAGGAGGACGCTCGTCGTGGCACCTCTGGCTTTCCCTCCATTTTGC 239
QY     21 LeuCysGlnaspLurytMetgLuserProGIInThrglyLeuProRoasPySer 40
       ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db     240 CTGTGTCAAATGAATACATGAGTGTCGCCAACAGCGGAGAGATGGCCCCACACTGACC 239
QY     41 LysCysGlyshisGLyAspTYrSerPheaRgelyTYTgInglyProProglyProProgly 60
       ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db     300 AAGTGTGGCCATGAGATTAATGTGATTCCGGGTGTACCAAGAGGGCCCCCTGGACCCCAGGT 359
QY     61 ProProglylleProglyAsnHisGLyAsnAsnGLyAsnAsnGLyAlahrglyHisGLu 80
       ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db     360 CTCCTCTGGCTTCCAGGAAACCATGGAAACAATGGAAATAAGGACCCACTGGCCCGCAA 419
QY     81 GLyAlaLysGLyluLysGLyAspLysGLyAspLeuGLyProArGLyGLuArGLyGLn 100
       ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db     420 GGGGCCCAAGGAGTGAAGAAGAGACAAAGCCGACTGGGGCTTCGAGGAGAACGGGGCAG 479
QY    101 HisGLyProLysGLyluLysGLyTYrProGLyileProProGLyluLeuGlnleAlape 120
       ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db     480 CATGGCCCCCAAGAAGATGAAGAGATCCACGAGGGTCCACAGAGAGTGCAGATTGCGTTCC 539
121 MetAlaSerIlemlaIahrhrlshpheserAasnGLyPaeRScrcLYTTLALRhSccscscLYn 140

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|   |   |   |
|---|---|---|
| KM  |   | inflammation; neurological disease; ss. |
| OS  | Rattus sp.  |   |
| PN  | M020069884-A2.  |   |
| XX  |   |   |
| PD  | 23-NOV-2000.  |   |
| PF  | 15-MAY-2000; 2000MO-NZ0075.   |   |
| PR  | 14-MAY-1999; 99US-0312283.  |   |
| XX  | (GENE-) GENESIS RES & DEV CORP LTD.   |   |
| PA  |   |   |
| PI  | Watson JD, Strachan L, Onurst R, Sleeman M, Kumble KD, Murison JG;  |   |
| XX  | WPI: 2001-007495/01.  |   |
| DR  | P-PSTDB: AAB55908.  |   |
| PS  | New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases -  |   |
| PT  |   |   |
| XX  | Claim 1; Page 87; 352pp; English.   |   |
| CC  | The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of oligonucleotides for examining expression patterns. |   |
| CC  |   |   |
| CX  |   |   |
| SQ  | Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other:  |   |
| Alignment Scores:                           |   |   |
| Pred. NO.:                                  | 3,36e-95  | Length: 1123                            |
| Score:                                      | 1311.00   | Matches: 236                            |
| Percent Similarity:                         | 97.15%  | Conservative: 3                         |
| Best Local Similarity:                      | 95.93%  | Mismatches: 7                           |
| Query Match:                                | 95.90%  | Indels: 0                               |
| DB:   | 22  | Gaps: 0                                 |
| US-10-036-041-2 (1-246) x AAC99566 (1-1123) |   |   |
| QY  | MetLeutPrArgInleuIetfyrTrpgInLeuAlaLephheLeuProPhcys 20<br>           :::   |   |
| Dd  | 180 ATGTCTACAGAGCGACTCCTGTGGTGCACCTCTGGCTTTTCCTCCATTTTGC 239  |   |
| QY  | 21 LeucSynaspJuryrMeUgUserProglInThrglyLeuProRoaspcySer 40<br>  |   |
| Dd  | 240 CTGTGTCAATGAATCATGATGAGTGTCGCCAACAGCGAGAATGGCCCCAAGCTCAC 239  |   |
| QY  | 41 LyscsyShsthsigLyAspyrSerpheaRgelyTyrglnGlyProbroglyProprogly 60<br>  |   |
| Dd  | 300 AAGTGTGCGCATGGAGATTGTGATTCCTCGGTACCAGAGGGCCCCTCGACCCCAAGGT 359  |   |
| QY  | 61 ProbroglylleProglyAsnHsigLYasnASGLYasnAnsgLYalahrGlyhlSiglu 80<br>   |   |
| Dd  | 360 CTCCTGTGCTTCAGAGAAACCATGGAAAACAATGGAATAACGACCCACGTGCCCGNA 419   |   |
| QY  | 81 GLYALALysGLylubLysGLYAspLysGLYAspLeuglYProargGLYLuargrGLYIn 100<br>  |   |
| Dd  | 420 GGggccCAAggGTGaGAAAGAGAGCAAAGCGAcACTGGgcctTCgaGgGAAAGGGGcAG 479   |   |
| QY  | 101 HisgilYProLysGLylubLysGLYTyrProglYlleProProglInleuGlnlealephe 120<br>   |   |
| Dd  | 480 CATGGCCCAAGGAAGTAAGAGATGCCACGAGGGTCCACAGAGGTGCAGATTGCgttc 539   |   |
| 121   | MetaLSerLeuAlahThrHispheserArnsnglYpacRscrClYrttAtLRhscscscvltja 140  |   |

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QY 21 LeucylGlnAspGluTyrMetGluSerProGlnThrGlyLeuProPheCysSer 40
    |||||
Db 240 CTGTGCAAGATTAATACATGAGTCTCCACAGCTGAGAGATGCCCCACAGCTCAGC 299
QY 41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProGlyProGly 60
    |||||
Db 300 AAGTGTTCATGAGATATGATTCGCTGATACCAAGGGCCCTGAGCCCCAGCT 359
QY 61 ProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
    |||||
Db 360 CCTCTGCGCATTCAGAGAAACCATGGAACAAATGAAATPACGAGCCACTGGCCGAA 419
QY 81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyLysGln 100
    |||||
Db 420 GGGGCCAAGGCTGAGAAAGAGACAAAGGAGACCTGGGCTCGAAGGAGAGCGGCGAG 479
QY 101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120
    |||||
Db 480 CAGGCCCCCAAGATAGAGAGGATACCCAGGGGTCCACAGAGCTGACAGATTGCGCTTC 539
QY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
    |||||
Db 540 ATGGCTTCTCTAGCGACTCATTCCACCAATCAGAACAGTGGCATTTCTTCACGCACTGTT 599
QY 141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
    |||||
Db 600 GAGACCAACATTCGAAACTTCTTCGATGTCATGACTGGTAGATTGGGGCCCCGATTA 659
QY 161 GlyValTyrPhePheThrPheSerMetMetLysHisGlyAspValGluGluValTyrVal 180
    |||||
Db 660 GCGGTATTCTTTCACCTTCACCATGATGATGATGATGATGATGATGATGATGATG 719
QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetLysSerTyrGluMetLysGlyLys 200
    |||||
Db 720 TACCTTATGCAACATGTAACAGCGTTCAGCATGTACATGATTAACCAAGGAGAAA 779
QY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPleu 220
    |||||
Db 780 TCAGATACATCCAGCAACCATGCACTGCTGAACTGGCCAAAGAGATGATGCTGCTA 839
QY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
    |||||
Db 840 AGAATGGGCAACGCTGCCCTCCATGCGGAGACCAACGCTTCTCTACCTCGCAGGCTTT 899
QY 241 LeuLeuPheGluThrLys 246
    |||||
Db 900 CTGCTTTTGAACCTAAG 917

RESULT 2
US-09-188-930-203
Sequence 203, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FASTSeq for Windows Version 3.0
SEQ ID NO 203
LENGTH: 1123
TYPE: DNA
ORGANISM: Rat
US-09-188-930-203
Alignment Scores:

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Pred. No.: 1,21e-117 Length: 1123
Score: 1311.00 Matches: 236
Percent Similarity: 97.15% Conservative: 3
Best Local Similarity: 95.93% Mismatches: 7
Query Match: 95.90% Indels: 0
DB: 3 Gaps: 0
US-10-036-041-2 (1-246) x US-09-188-930-203 (1-1123)

QY 1 MetLeuTPArgGlnLeuIleTyrTrpGlnLeuAlaLeuPheLeuProPheCys 20
    |||||
Db 180 AAGCTCAGAGAGACAGCTGCTGAGGACACCTGCGCTTTCCTTCTCCATTTGCG 239
QY 21 LeucylGlnAspGluTyrMetGluSerProGlnThrGlyLeuProPheCysSer 40
    |||||
Db 240 CTGTGCAAGATTAATACATGAGTCTCCACAGCTGAGAGATGCCCCACAGCTCAGC 299
QY 41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProGlyProGly 60
    |||||
Db 300 AAGTGTTCATGAGATATGATTCGCTGATACCAAGGGCCCTGAGCCCCAGCT 359
QY 61 ProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
    |||||
Db 360 CCTCTGCGCATTCAGAGAAACCATGGAACAAATGAAATPACGAGCCACTGGCCGAA 419
QY 81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyLysGln 100
    |||||
Db 420 GGGGCCAAGGCTGAGAAAGAGACAAAGGAGACCTGGGCTCGAAGGAGAGCGGCGAG 479
QY 101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120
    |||||
Db 480 CAGGCCCCCAAGATAGAGAGGATACCCAGGGGTCCACAGAGCTGACAGATTGCGCTTC 539
QY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
    |||||
Db 540 ATGGCTTCTCTAGCGACTCATTCCACCAATCAGAACAGTGGCATTTCTTCACGCACTGTT 599
QY 141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
    |||||
Db 600 GAGACCAACATTCGAAACTTCTTCGATGTCATGACTGGTAGATTGGGGCCCCGATTA 659
QY 161 GlyValTyrPhePheThrPheSerMetMetLysHisGlyAspValGluGluValTyrVal 180
    |||||
Db 660 GCGGTATTCTTTCACCTTCACCATGATGATGATGATGATGATGATGATGATG 719
QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetLysSerTyrGluMetLysGlyLys 200
    |||||
Db 720 TACCTTATGCAACATGTAACAGCGTTCAGCATGTACATGATTAACCAAGGAGAAA 779
QY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPleu 220
    |||||
Db 780 TCAGATACATCCAGCAACCATGCACTGCTGAACTGGCCAAAGAGATGATGCTGCTA 839
QY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
    |||||
Db 840 AGAATGGGCAACGCTGCCCTCCATGCGGAGACCAACGCTTCTCTACCTCGCAGGCTTT 899
QY 241 LeuLeuPheGluThrLys 246
    |||||
Db 900 CTGCTTTTGAACCTAAG 917

RESULT 3
US-09-188-930-217
Sequence 217, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells

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